

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Escobedo, Jaime
Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Srinivas
- (ii) TITLE OF THE INVENTION: Secreted Human Proteins
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Witcoff
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 11-DEC-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/032757
(B) FILING DATE: 11-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32141
(C) REFERENCE/DOCKET NUMBER: 2441.39505
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2063 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA	CGAGGCCTCA	GTCTTCCAGG	GCGGCGGTGG	GTGTCCGCTT	CTCTCTGCTC	60
TTCGACTGCA	CCGCACTCGC	GCGTGACCCT	GACTCCCCCT	AGTCAGCTCA	GCGGTGCTGC	120
CATGGCGTGG	CGGCGGCGCG	AAGCCGGCGT	CGGGGCTCGC	GGCGTGTGG	CTCTGGCGTT	180
GCTCGCCCTG	GCCCTGTGCG	TGCCCCGGGG	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTGGA	GCGTCTCGGA	300
GAGTGGCCGC	TTCGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
GTGGGCGCCC	GGCGGAGACC	TCGAGGGCTG	CGCGCCCGAC	ACGCGCTTCT	TCGTGCCCCG	420
GCCCCGGCGC	CGAGGGGCGG	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
CAAGGACAAG	GTGCTGGTGG	CGGCGCGGAG	GAACGCCTCG	GCCGTCGTCC	TCTACAATGA	540
GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAACAGGAA	ATATAGTGGT	600
CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTTCATCA	GCGGTCAGTC	720
TGTGGTGTTT	GTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
ATTTTACTAT	ATACAGCGTT	TCCTATATAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
AAAAGAAACT	AAGAAAGTTA	TTGGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
GGGAATTGAT	GTTGATGCTG	AAAATTGTGC	AGTGTGTATT	GAAAATTTCA	AAGTAAAGGA	960
TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
TTTGGATCAC	CGAACATGTC	CAATGTGTAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
GGGAGAGCCT	GGGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
AGCTGCAAAT	TTGAGTCTAG	CTTTACCAGA	TGATGACGGA	AGTGATGACA	GCAGTCCACC	1200
ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
AGAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGACTCT	CGGCATGGAG	GACCCATCTC	1320
CTAGCACACG	TGCCCCACTGA	AGTGGCACCA	ACAGAAGTTT	GGCTTGAAC	AAAGGACATT	1380
TTATTTTTTT	TACTTTAGCA	CATAATTTGT	ATATTTGAAA	ATAATGTATA	TTATTTTACC	1440
TATTAGATTC	TGATTTGATA	TACAAAGGAC	TAAGATATTT	TCTTCTTGAA	GAGACTTTTC	1500
GATTAGTCCT	CATATATTTA	TCTACTAAAA	TAGAGTGTTT	ACCATGAACA	GTGTGTTGCT	1560
TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	TAAAGGACAG	GTGGTGTTTC	1620
TAAATAATTG	GCTGCTATGG	TTCTGTAAAA	ACCAGTTAAT	TCTATTTTTC	AAGGTTTTTG	1680
GCAAAGCACA	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
ATCTCATGGG	CTTTCCCTGG	AGGAAAGGTT	TTTTTTGTTG	TTTTTTTTTT	AAGAACTTGA	1800
AACTTGTAAG	CTGAGATGTC	TGTAGCTTTT	TTGCCCATCT	GTAGTGTATG	TGAAGATTTC	1860
AAAACCTGAG	AGCACTTTTT	CTTTGTTT	AGATTATGAGA	AAGGCACTAG	ATGACTTTAG	1920
GATTTGCATT	TTTCCCTTTA	TTGCCTCATT	TCTTGTGACG	CCTTGTTGGG	GAGGGAAATC	1980
TGTTTATTTT	TTCTACAAA	TAAAAAGCTA	AGATTCTATA	TCGCAAAAAA	AAAAAAAAAA	2040
AAAAAAAAAA	TTCCTGCGGC	CGC				2063

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCA	CGAGGTAGGC	AAGGGATAAA	AAGGCACCTA	AGGCCCTTTT	GCAATAAGAA	60
GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTTGG	GGAAGGTCCC	120

CGGCCCCCAC	AGCCCTCTGG	GGAGCCTCAC	CCTGGCTCTC	CCCACTCACC	TCAGCCCTCA	180
GGCAGCCCCT	CCACAGGGCC	CCTCTCCTGC	CTGGACAGCT	CTGCTGGTCT	CCCCGTCCCC	240
TGGAGAAGAA	CAAGGCCATG	GGTCGGCCCC	TGCTGCTGCC	CCTGCTGCTC	CTGCTGCAGC	300
CGCCAGCATT	TCTGCAGCCT	GGTGGCTCCA	CAGGATCTGG	TCCAAGCTAC	CTTTATGGGG	360
TCACTCAACC	AAAACACCTC	TCAGCCTCCA	TGGGTGGCTC	TGTGGAAATC	CCCTTCTCCT	420
TCTATTACCC	CTGGGAGTTA	GCCATAGTTC	CCAACGTGAG	AATATCCTGG	AGACGGGGCC	480
ACTTCCACGG	GCAGTCCTTC	TACAGCACAA	GGCCGCCTTC	CATTCACAAG	GATTATGTGA	540
ACCGGCTCTT	TCTGAACTGG	ACAGAGGGTC	AGGAGAGCGG	CTTCCTCAGG	ATCTCAAACC	600
TGCGGAAGGA	GGACCAGTCT	GTGTATTTCT	GCCGAGTCGA	GCTGGACACC	CGGAGATCAG	660
GGAGGCAGCA	GTTGCAGTCC	ATCAAGGGGA	CCAACTCAC	CATCACCAG	GCTGTCACAA	720
CCACCACCAC	CTGGAGGCCC	AGCAGCACAA	CCACCATAGC	CGGCCTCAGG	GTCACAGAAA	780
GCAAAGGGCA	CTCAGAATCA	TGGCACCTAA	GTCTGGACAC	TGCCATCAGG	GTTGCATTGG	840
CTGTGCTGT	GCTCAAAACT	GTCATTTTGG	GACTGCTGTG	CCTCCTCCTC	CTGTGGTGGA	900
GGAGAAGGAA	AGGTAGCAGG	GCGCCAAGCA	GTGACTTCTG	ACCAACAGAG	TGTGGGGAGA	960
AGGGATGTGT	ATTAGCCCCG	GAGGACGTGA	TGTGAGACCC	GCTTGTGAGT	CCTCCACACT	1020
CGTTCCCCAT	TGGCAAGATA	CATGGAGAGC	ACCCTGAGGA	CCTTTAAAAG	GCAAAGCCGC	1080
AAGGCAGAAG	GAGGCTGGGT	CCCTGAATCA	CCGACTGGAG	GAGAGTTACC	TACAAGAGCC	1140
TTCATCCAGG	AGCATCCACA	CTGCAATGAT	ATAGGAATGA	GGTCTGAACT	CCACTGAATT	1200
AAACCACTGG	CATTTGGGGG	CTGTTTATTA	TAGCAGTGCA	AAGAGTTCCT	TTATCCTCCC	1260
CAAGGATGGA	AAAATACAAT	TTATTTTGCT	TACCATAAAA	AAAAAAAAAA	AAAAATTCCT	1320
GCGGCCGC						1328

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGGCA	CGAGGGCAAG	ATTCGATACA	AAACCAATGA	ACCTGTGTGG	GAGGAAAAC	60
TCACCTTCTT	CATTCACAAT	CCCAAGCGCC	AGGACCTTGA	AGTTGAGGTC	AGAGACGAGC	120
AGCACCAGTG	TTCCCTGGGG	AACCTGAAGG	TCCCCCTCAG	CCAGCTGCTC	ACCAGTGAGG	180
ACATGACTGT	GAGCCAGCGC	TTCCAGCTCA	GTAACCTCGG	TCCAACAGC	ACCATCAAGA	240
TGAAGATTGC	CCTGCGGGTG	CTCCATCTCG	AAAAGCGAGA	AAGGCCTCCA	GACCACCAAC	300
ACTCAGCTCA	AGTCAAACGT	CCCTCTGTGT	CCAAAGAGGG	GAGGAAAACA	TCCATCAAAT	360
CTCATATGTC	TGGGTCTCCA	GGCCCTGGTG	GCAGCAACAC	AGCTCCATCC	ACACCAGTCA	420
TTGGGGGCGAG	TGATAAGCCT	GGTATGGAAG	AAAAGGCCCA	GCCCCCTGAG	GCCGGCCCTC	480
AGGGGCTGCA	CGACCTGGGC	AGAAGCTCCT	CCAGCCTCCT	GGCCTCCCCA	GGCCACATCT	540
CAGTCAAGGA	GCCGACCCCC	AGCATCGCCT	CGGACATCTC	GCTGCCCATC	GCCACCCAGG	600
AGCTGCGGCA	AAGGCTGAGG	CAGCTGGAAA	ACGGGACGAC	CCTGGGACAG	TCTCCACTGG	660
GGCAGATCCA	GCTGACCATC	CGGCACAGCT	CGCAGAGAAA	CAAGCTTATC	GTGGTCGTGC	720
ATGCCTGCAG	AAACCTCATT	GCCTTCTCTG	AAGACGGCTC	TGACCCCTAT	GTCCGCATGT	780
ATTTATTACC	AGACAAGAGG	CGGTCAGGAA	GGAGGAAAAC	ACACGTGTCA	AAGAAAACAT	840
TAAATCCAGT	GTTTGATCAA	AGCTTTGATT	TCAGTGTTTC	GTTACCAGAA	GTGCAGAGGA	900
GAACGCTCGA	CGTTGCCGTG	AAGAACAGTG	GCGGCTTCCT	GTCCAAAGAC	AAAGGGCTCC	960
TTGGCAAAGT	ATTGGTTGCT	CTGGCATCTG	AAGAACTTGC	CAAAGGCTGG	ACCCAGTGGT	1020
ATGACCTCAC	GGAAGATGGG	ACGAGGCCTC	AGGCGATGAC	ATAGCCGCAG	CAGGCAGGAG	1080
GCGTCCTCTT	CAGCGTAGCT	CTCCACCTCT	ACCCGGAACA	CACCCTCTCA	CAGACGTACC	1140
AATGTTATTT	TTATAATTTC	ATGGATTTAG	TTATACATAC	CTTAATAGTT	TTATAAAATT	1200
GTTGACATTT	CAGGCAAATT	TGGCCAATAT	TATCATTGAA	TTTTCTGTGT	TGGATTTCTT	1260
CTAGGATTTT	GCCAGTTCTT	ACAACGTGCA	GTAGGGCGGC	GGTAGCTCTT	GTGTCTGTGG	1320
ACTCTGCTCA	GCTGTGTCCG	TAGGAGTCGG	ATGTGTCTGT	GCTTTATTAT	GGCCTTGTTT	1380
ATATATCACT	GAGGTATACT	ATGCCATGTA	AATAGACTAT	TTTTTATAAT	CTTAACATGC	1440

TGGTTTAAAT	TCAGAAGGAA	ATAGATCAAG	GAAATATATA	TATTTTCTTC	TAAAACTTAT	1500
TAAATTCGTG	TGACAAATAA	TCATTTTCAT	CTTGGCAGCA	AAAAGTTCTC	AGTGACCTAT	1560
TTTGTGGTGT	TTCTTTTGA	AAAGAAAAGC	TGAAATATTA	TTAAATGCTA	GTATGTTTCT	1620
GCCCATTATG	AAAGATGAAA	TAAAGTATTC	AAAATATTAA	AAAAAAAAAA	AAAAAATTCC	1680
TGCGGCCCGC						1689

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCA	CGAGGAGCAG	ATCTGCAAGA	GTTTCGTTTA	TGGAGGCTGC	TTGGGCAACA	60
AGAACAACCTA	CCTTCGGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTG	CAAGGTGGGC	120
CTTTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTTCCCCCA	GGGCCCCTCC	ATGGAAAGGC	180
GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
GCATCGACAG	TTTCCTGGAG	TGTGACGACA	CCCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
CTGCCTGTGA	AAAATACACG	AGTGGCTTTG	ACGAGCTCCA	GCGCATCCAT	TTCCCCAGCG	360
ACAAAGGGCA	CTGCGTGGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCGCGCT	420
GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCGCTTTAC	CTATGGTGGT	TGTTACGGCA	480
ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTGCGGCG	ATCTCCAAGA	540
AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
CTGTGCGAGT	GTTCTGGTC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTTACTGCT	660
TCTTCAAGAA	CCAGAGAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
CCAGCTCCAC	TGTCTCCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
GGCCCCTCTG	AGCCTGGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
CAGAGGCCTG	GGCTGGGAAA	AACTTTGGAA	CCAGACTCTT	GCCTGTTTCC	CAGGCCCACT	900
GTGCCTCAGA	GACCAGGGCT	CCAGCCCCTC	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCCT	960
GAGAAAGCTC	AAAGGTTTGG	AAGGAGCAGA	AAACCCTTGG	GCCAGAAGTA	CCAGACTAGA	1020
TGGACCTGCC	TGCATAGGAG	TTTGGAGGAA	GTTGGAGTTT	TGTTTCCTCT	GTTCAAAGCT	1080
GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTGAGAC	CCTGGAGGCC	1140
CCAACCCTGT	CCTCCCGAGC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
TTCCCTGTGT	AGTTTGTGCT	GTAAAGAGTT	GCTTTTTGTT	TATTTAATGC	TGTGGCATGG	1260
GTGAAGAGGA	GGGAAGAGG	CCTGTTTGGC	CTCTCTATCC	TCTCTTCCTC	TTCCCCAAG	1320
ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
GAAGCTCAGC	TGCATTCCGC	AGCCCCCACC	CCCAAGGTTT	TCCAACATCA	CAGCCCAGCC	1440
CGCCCCTG	GTAATAAAAG	TGGTTTGTGG	AAAAAAAAAA	AAAAAAAAAA	AAGTCCTGCG	1500
GCCGC						1505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTGCG	CCGCGCGGGG	TCGCGGCGGC	120

CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
GCGGCGCGCG	TGGCCCGCTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
TCCACGCTGG	AGGCGGTGCG	CGGCCGGCCC	TTCGCCGACG	TCCTCTCGCT	CAGCGACGGG	300
CCCCCGGGCG	CGGGCAGCGG	CGTGCCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
AGCAACCTGC	AGGAGAATCC	ATATGCTACA	CTGACCATGA	CTTTGGCACA	GACCAACTTC	420
TGCAAGAAAC	ATGGATTTGA	TCCACAAAGT	CCCCTTTGTG	TTCACATAAT	GCTGTCAGGA	480
ACTGTGACCA	AGGTGAATGA	AACAGAAATG	GATATTGCAA	AGCATTCGTT	ATTCATTCTGA	540
CACCCTGAGA	TGAAAACCTG	GCCTTCCAGC	CATAATTGGT	TCTTTGCTAA	GTTGAATATA	600
ACCAATATCT	GGGTCCCTGGA	CTACTTTGGT	GGACCAAAAA	TCGTGACACC	AGAAGAATAT	660
TATAATGTCA	CAGTTCAGTG	AAGCAGACTG	TGGTGAATTT	AGCAACACTT	ATGAAGTTTC	720
TTAAAGTGGC	TCATACACAC	TTAAAAGGCT	TAATGTTTCT	CTGGAAAGCG	TCCCAGAATA	780
TTAGCCAGTT	TTCTGTCACA	TGCTGGTTTG	TTTGCTTGCT	TGTTTACTTG	CTTGTTTACC	840
AATAGAGTTG	ACCTGTTATT	GGATTTCTTG	GAAGATGTGG	TAGCTACTTT	TTTCCCTATTT	900
TGAAGCCATT	TTCTGATAGA	AATATCCTTC	ACTATAATCA	AATAAGTTTT	GTCCCATCAA	960
TTCCAAAGAT	GTTTCCAGTG	GTGCTCTTGA	AGAGGAATGA	GTACCAGTTT	TAAATTGCCC	1020
ATTGGCATT	GAAGGTAGTT	GAGTATGTGT	TCTTTATTCC	TAGAAGCCAC	TGTGCTTGGT	1080
AGAGTGCATC	ACTCACCACA	GCTGCCTCTT	GAGCTGCCTG	AGCCTGGTGC	AAAAGGATTG	1140
GCCCCCATTA	TGGTGCTTCT	GAATAAATCT	TGCCAAGATA	GACAAACAAT	GATGAAACTC	1200
AGATGGAGCT	TCCTACTCAT	GTTGATTTAT	GTCTCACAAT	CCTGGGTATT	GTTAATTCAA	1260
CATAGGGTGA	AACTATTTCT	GATAAAGAAC	TTTTGAAAAA	CTTTTTTATAC	TCTAAAGTGA	1320
TACTCAGAAC	AAAAGAAAGT	CATAAAACTC	CTGAATTTAA	TTTCCCCACC	TAAGTCGAGA	1380
CAGTATTATC	AAAACACATG	TGCACACAGA	TTATTTTTTG	GCTCCAAAAC	TGGATTGCAA	1440
AAGAAAGAGG	AGAGATATTT	TGTGTGTTCC	TGGTATTCTT	TTATAAGTAA	AGTTACCCAG	1500
GCATGGACCA	GCTTCAGCCA	GGGACAAAAT	CCCCTCCCAA	ACCACTCTCC	ACAGCTTTTT	1560
AAAAATACTT	CTACTCTTAA	CAATTACCTA	AGGTTCCCTC	AAACCCCCC	AACTCTTAAT	1620
AGCTTCTAGT	GCTGCTACAA	TCTAAGTCAG	GTCACCAGAG	GGAAGAGAAC	ATGGCATTAA	1680
AAGAATCACA	TCTTCAGAAG	AGAAGACACT	AATATTATTA	CCCATATACA	TGATTTTCAGA	1740
AGATGACATA	AGATTCCTCT	TAAAGAGGAA	ATGTCAGGAA	TCAAGCCACT	GAATCCTTAA	1800
AGAGAAAAGT	TGAATATGAG	TCATTGTGTC	TGAAAACCTG	AAAGTGAAC	TAAGTGAGAT	1860
CCAGCAAACA	GGTTCTGTTT	AAGAAAAATA	ATTTATACTA	AATTTAGTAA	AATGGACTTC	1920
TTATTCAAAG	CATCAATAAT	TAAAAGAATT	ATTTTAAAAA	AAAAAAAAAA	AAAAAAAAAA	1980
AAAAAAAAAT	TCCTGCGGCC	GC				2002

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGCA	CGAGGGCCAC	GACTCTGCTG	GCATTTCTTC	TATAGCCACT	GGAATCTGAT	60
CCTGATTGTC	TTCCACTACT	ACCAGGCCAT	CACCACTCCG	CCTGGGTACC	CACCCCAGGG	120
CAGGAATGAT	ATCGCCACCG	TCTCCATCTG	TAAGAAGTGC	ATTTACCCCA	AGCCAGCCCG	180
AACACACCAC	TGCAGCATCT	GCAACAGGTG	TGTGCTGAAG	ATGGATCACC	ACTGCCCCTG	240
GCTAAACAAT	TGTGTGGGCC	ACTATAACCA	TCGGTACTTC	TTCTCTTTCT	GCTTTTTTCAT	300
GACTCTGGGC	TGTGTCTACT	GCAGCTATGG	AAGTTGGGAC	CTTTTCCGGG	AGGCTTATGC	360
TGCCATTGAG	AAAATGAAAC	AGCTCGACAA	GAACAAACTA	CAGGCGGTG	CCAACCAGAC	420
TTATCACCAG	ACCCACCCAC	CCACCTTCTC	CTTTCGAGAA	AGGATGACTC	ACAAGAGTCT	480
TGTCTACCTC	TGGTTCCTGT	GCAGTTCTGT	GGCACTTGCC	CTGGGTGCCC	TAACTGTATG	540
GCATGCTGTT	CTCATCAGTC	GAGGTGAGAC	TAGCATCGAA	AGGCACATCA	ACAAGAAGGA	600
GAGACGTCGG	CTACAGGCCA	AGGGCAGAGT	ATTTAGGAAT	CCTTACAAC	ACGGCTGCTT	660
GGACAACCTG	AAGGTATTCC	TGGGTGTGGA	TACAGGAAGG	CACTGGCTTA	CTCGGGTGCT	720
CTTACCTTCT	ACTCACTTGC	CCCATGGGAA	TGGAATGAGC	TGGGAGCCCC	CTCCCTGGGT	780

GACTGCTCAC	TCAGCCTCTG	TGATGGCAGT	GTGAGCTGGA	CTGTGTCAGC	CACGACTCGA	840
GCACTCATTC	TGCTCCCTAT	GTTATTTCAA	GGGCCTCCAA	GGGCAGCTTT	TCTCAGAATC	900
CTTGATCAAA	AAGAGCCAGT	GGGCCTGCCT	TAGGGTACCA	TGCAGGACAA	TTCAAGGACC	960
AGCCTTTTTA	CCACTGCAGA	AGAAAGACAC	AATGTGGAGA	AATCTTAGGA	CTGACATCCC	1020
TTTACTCAGG	CAAACAGAAG	TTCCAACCCC	AGACTAGGGG	TCAGGCAGCT	AGCTACCTAC	1080
CTTGCCCAGT	GCTGACCCGG	ACCTCCTCCA	GGATACAGCA	CTGGAGTTGG	CCACCACCTC	1140
TTCTACTTGC	TGTCTGAAAA	AACACCTGAC	TAGTACAGCT	GAGATCTTGG	CTTCTCAACA	1200
GGGCAAAGAT	ACCAGGCCTG	CTGCTGAGGT	CACTGCCACT	TCTCACATGC	TGCTTAAGGG	1260
AGCACAAATA	AAGGTATTCG	ATTTTAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCA	CGAGGAGCCT	GCCTTCATCT	AGGATGGCTC	CTCTGGGCAT	GCTGCTTGGG	60
CTGCTGATGG	CCGCCTGCTT	CACCTTCTGC	CTCAGTCATC	AGAACCTGAA	GGAGTTTGCC	120
CTGACCAACC	CAGAGAAGAG	CAGCACCAAA	GAAACAGAGA	GAAAAGAAAC	CAAAGCCGAG	180
GAGGAGCTGG	ATGCCGAAGT	CCTGGAGGTG	TTCCACCCGA	CGCATGAGTG	GCAGGCCCTT	240
CAGCCAGGGC	AGGCTGTCCC	TGCAGGATCC	CACGTACGGC	TGAATCTTCA	GACTGGGGAA	300
AGAGAGGCAA	AACTCCAATA	TGAGGACAAG	TTCCGAAATA	ATTTGAAAGG	CAAAGGCTG	360
GATATCAACA	CCAACACCTA	CACATCTCAG	GATCTCAAGA	GTGCACTGGC	AAAATTCAAG	420
GAGGGGGCAG	AGATGGAGAG	TTCAAAGGAA	GACAAGGCAA	GGCAGGCTGA	GGTAAAGCGG	480
CTCTTCCGCC	CCATTGAGGA	ACTGAAGAAA	GACTTTGATG	AGCTGAATGT	TGTCATTGAG	540
ACTGACATGC	AGATCATGGT	ACGGCTGATC	AACAAGTTCA	ATAGTTCCAG	CTCCAGTTTG	600
GAAGAGAAGA	TTGCTGCGCT	CTTTGATCTT	GAATATTATG	TCCATCAGAT	GGACAATGCG	660
CAGGACCTGC	TTTCCTTTGG	TGGTCTTCAA	GTGGTGATCA	ATGGGCTGAA	CAGCACAGAG	720
CCCCTCGTGA	AGGAGTATGC	TGCGTTTGTG	CTGGGCGCTG	CCTTTTCCAG	CAACCCCAAG	780
GTCCAGGTGG	AGGCCATCGA	AGGGGGAGCC	CTGCAGAAGC	TGCTGGTCAT	CCTGGCCACG	840
GAGCAGCCGC	TCACTGCAAA	GAAGAAGGTC	CTGTTTGCAC	TGTGCTCCCT	GCTGCGCCAC	900
TTCCCCTATG	CCCAGCGGCA	GTTCTTGAAG	CTCGGGGGGC	TGCAGGTCCT	GAGGACCCTG	960
GTGCAGGAGA	AGGGCACGGA	GGTGCTCGCC	GTGCGCGTGG	TCACACTGCT	CTACGACCTG	1020
GTCACGGAGA	AGATGTTTCG	CGAGGAGGAG	GCTGAGCTGA	CCCAGGAGAT	GTCCCCAGAG	1080
AAGCTGCAGC	AGTATCGCCA	GGTACACCTC	CTGCCAGGCC	TGTGGGAACA	GGGCTGGTGC	1140
GAGATCACGG	CCCACCTCCT	GGCGCTGCCC	GAGCATGATG	CCCGTGAGAA	GGTGCTGCAG	1200
ACACTGGGCG	TCCTCCTGAC	CACCTGCCGG	GACCGCTACC	GTCAGGACCC	CCAGCTCGGC	1260
AGGACACTGG	CCAGCCTGCA	GGCTGAGTAC	CAGGTGCTGG	CCAGCCTGGA	GCTGCAGGAT	1320
GGTGAGGACG	AGGGCTACTT	CCAGGAGCTG	CTGGGCTCTG	TCAACAGCTT	GCTGAAGGAG	1380
CTGAGATGAG	GCCCCACACC	AGGACTGGAC	TGGGATGCCG	CTAGTGAGGC	TGAGGGGTGC	1440
CAGCGTGGGT	GGGCTTCTCA	GGCAGGAGGA	CATCTTGGCA	GTGCTGGCTT	GGCCATTAAA	1500
TGGAAACCTG	AAGGCCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1560
TTCTTGC	CGC					1573

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGGGGGCT	TTAAGGGACA	GCTGAGCCGG	CAGGTGGCAG	ATCAGATGTG	60
GCAGGCTGGG	AAAAGACAAG	CCTCCAGGGC	CTTCAGCTTG	TACGCCAACA	TCGACATCCT	120
CAGACCCTAC	TTTGATGTGG	AGCCTGCTCA	GGTGCGAAGC	AGGCTCCTGG	AGTCCATGAT	180
CCCTATCAAG	ATGGTCAACT	TCCCCCAGAA	AATTGCAGGT	GAAGTCTATG	GACCTCTCAT	240
GCTGGTCTTC	ACTCTGGTTG	CTATCCTACT	CCATGGGATG	AAGACGTCTG	ACACTATTAT	300
CCGGGAGGGC	ACCCTGATGG	GCACAGCCAT	TGGCACCTGC	TTCGGCTACT	GGCTGGGAGT	360
CTCATCCTTC	ATTTACTTCC	TTGCCTACCT	GTGCAACGCC	CAGATCACCA	TGCTGCAGAT	420
GTTGGCACTG	CTGGGCTATG	GCCTCTTTGG	GCATTGCATT	GTCCTGTTCA	TCACCTATAA	480
TATCCACCTC	CACGCCCTCT	TCTACCTCTT	CTGGCTGTTG	GTGGGTGGAC	TGTCCACACT	540
GCGCATGGTA	GCAGTGTGG	TGTCTCGGAC	CGTGGGCCCC	ACACAGCGGC	TGCTCCTCTG	600
TGGCACCTTG	GCTGCCCTAC	ACATGCTCTT	CCTGCTCTAT	CTGCATTTTG	CCTACCACAA	660
AGTGGTAGAG	GGGATCCTGG	ACACACTGGA	GGGCCCCAAC	ATCCCGCCCA	TCCAGAGGGT	720
CCCCAGAGAC	ATCCCTGCCA	TGCTCCCTGC	TGCTCGGCTT	CCCACCACCG	TCCTCAACGC	780
CACAGCCAAA	GCTGTTGCGG	TGACCCTGCA	GTCACACTGA	CCCCACCTGA	AATTCTTGGC	840
CAGTCCTCTT	TCCCGCAGCT	GCAGAGAGGA	GGAAGACTAT	TAAAGGACAG	TCCTGATGAC	900
ATGTTTCGTA	GATGGGGTTT	GCAGCTGCCA	CTGAGCTGTA	GCTGCGTAAG	TACCTCCTTG	960
ATGCCTGTCG	GCACTTCTGA	AAGGCACAAG	GCCAAGAAGT	CCTGGCCAGG	ACTGCAAGGC	1020
TCTGCAGCCA	ATGCAGAAAA	TGGGTCAGCT	CCTTTGAGAA	CCCCTCCCCA	CCTACCCCTT	1080
CCTTCCTCTT	TATCTCTCCC	ACATTGTCTT	GCTAAATATA	GACTTGGTAA	TTAAAATGTT	1140
GATTGAAGTC	TGGAAAAAAA	AAAAAAAAAA	AATTCCTGCG	GCCGC		1185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA	CGAGGCAAGC	CACCATCTTC	CTTCGGCCTG	CACCCCTTTA	AAGGCACCCA	60
GACCCCTCTG	GAAAAAGATG	AACTGAAGCC	CTTTGACATC	CTCCAGCCTA	AGGAGTACTT	120
CCAGCTCAGC	CGCCACACGG	TCATTAAGAT	GGGAAGTGAG	AACGAGGCCC	TGGATCTCTC	180
CATGAAGTCA	GTGCCCTGGC	TCAAGGCTGG	TGAAGTCAGT	CCCCCAATCT	TCCAGGAAGA	240
TGCAGCCCTA	GACCTGTCAG	TGGCAGCCCA	CCGGAAATCC	GAGCCTCCCC	CTGAGACACT	300
GTATGACAGT	GGTGCATCAG	TGGACAGCTC	AGGTCACACA	GTGATGGAGA	AACTTCCCAG	360
TGGCATGGAA	ATTTCTTTTG	CCCCTGCCAC	GTCCCATGAG	GCCCCAGCCA	TGATGGATAG	420
TCACATCAGC	AGCAGTGATG	CTGCTACCGA	GATGCTCAGC	CAGCCCAACC	ACCCAGCGG	480
CGAAGTCAAG	GCTGAAAATA	ACATTGAGAT	GGTGGGCGAG	TCCCAGGCGG	CCAAGGTCAT	540
TGTCTCTGTC	GAAGATGCTG	TGCCTACCAT	ATTCTGTGGC	AAGATCAAAG	GCCTCTCAGG	600
GGTGTCCACC	AAAAACTTCT	CCTTCAAAAG	AGAAGACTCC	GTGCTTCAGG	GCTATGACAT	660
CAACAGCCAA	GGGAAGAGT	CCATGGGAAA	TGCAGAGCCC	CTTAGGAAAC	CCATCAAAAA	720
CCGGAGCATA	AAGTTAAAGA	AAGTGAAGTC	CCAGGAAGTA	CACATGCTCC	CAATCAAAAA	780
ACAACGGCTG	GCCACCTTTT	TTCCAAGAAA	GTAAATAACG	GCTTTTTTAA	ATTTGTATGA	840
TTATAATATG	GGGAAGGTG	CATTGGTTTT	ATAAAAAGGC	ATTTAAAACA	AATTATCTTT	900
GTTAATTATT	TTGGGGAGTA	GTTGGGAAAT	GGAAAGGTGA	ATTGGCTCTA	GAGGCCCTGT	960
ATGCTAGTAT	CATTTTCTTT	TTTAATTTTT	GACTTTTCAC	AAATGAGTAA	ATAAGAGCAA	1020
CCTATTTTTC	AAGCAGATTG	CACATTTTTT	GCAGCTTTAA	TGGAATATTG	GGTGAATTAG	1080
AGGGGTAAAA	AAAGCTATTT	TCATTGCCAC	AAAGTGCTTT	GATGATGTAA	TACCTAATAA	1140
AGGGTAGGAT	GAATATTTCA	CAATAAATGT	TTGTTTGCAC	TAAAAAATAA	AAAAAATAA	1200
AAAAAATAA	AAATTCCTGC	GGCCGC				1226

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCA	CGAGGGCGCC	ATGGTGAAGG	TGACGTTCAA	CTCCGCTCTG	GCCCAGAAGG	60
AGGCCAAGAA	GGACGAGCCC	AAGAGCGGCG	AGGAGGCGCT	CATCATCCCC	CCCGACGCCG	120
TCGCGGTGGA	CTGCAAGGAC	CCAGATGATG	TGGTACCAGT	TGGCCAAAGA	AGAGCCTGGT	180
GTTGGTGCAT	GTGCTTTGGA	CTAGCATTTA	TGCTTGCAGG	TGTTATTCTA	GGAGGAGCAT	240
ACTTGTACAA	ATATTTTGCA	CTTCAACCAG	ATGACGTGTA	CTACTGTGGA	ATAAAGTACA	300
TCAAAGATGA	TGTCATCTTA	AATGAGCCCT	CTGCAGATGC	CCCAGCTGCT	CTCTACCAGA	360
CAATTGAAGA	AAATATTAAA	ATCTTTGAAG	AAGAAGAAGT	TGAATTTATC	AGTGTGCCTG	420
TCCCAGAGTT	TGCAGATAGT	GATCCTGCCA	ACATTGTTCA	TGACTTTAAC	AAGAAACTTA	480
CAGCCTATTT	AGATCTTAAC	CTGGATAAGT	GCTATGTGAT	CCCTCTGAAC	ACTTCCATTG	540
TTATGCCACC	CAGAAACCTA	CTGGAGTTAC	TTATTAACAT	CAAGGCTGGA	ACCTATTTGC	600
CTCAGTCCTA	TCTGATTCAT	GAGCACATGG	TTATTACTGA	TCGCATTGAA	AACATTGATC	660
ACCTGGGTTT	CTTTATTTAT	CGACTGTGTC	ATGACAAGGA	AACTTACAAA	CTGCAACGCA	720
GAGAAACTAT	TAAAGGTATT	CAGAAACGTG	AAGCCAGCAA	TTGTTTCGCA	ATTCGGCATT	780
TTGAAAACAA	ATTTGCCGTG	GAAACTTTAA	TTTGTTCTTG	AACAGTCAAG	AAAAACATTA	840
TTGAGGAAAA	TTAATATCAC	AGCATAACCC	CACCCTTTAC	ATTTTGTTGC	AGTTGATTAT	900
TTTTTAAAGT	CTTCTTTCAT	GTAAGTAGCA	AACAGGGCTT	TACTATCTTT	TCATCTCATT	960
AATTCAATTA	AAACCATTAC	CTTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1020
AAAAAAAAAA	AAAAAATTCC	TGCGGCCCGC				1049

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCGGCA	CGAGGGGAGA	ATACTTTTGT	CGATGCCTAC	TGGAGACTTT	GATTCGAAGC	60
CCAGTTGGGC	CGACCAGGTG	GAGGAGGAGG	GGGAGGACGA	CAAATGTGTC	ACCAGCGAGC	120
TCCTCAAGGG	GATCCCTCTG	GCCACAGGTG	ACACCAGCCC	AGAGCCAGAG	CTACTGCCGG	180
GAGCTCCACT	GCCGCCTCCC	AAGGAGGTCA	TCAACGGAAA	CATAAAGACA	GTGACAGAGT	240
ACAAGATAGA	TGAGGATGGC	AAGAAGTTCA	AGATTGTCCG	CACCTTCAGG	ATTGAGACCC	300
GGAAGGCTTC	AAAGGCTGTC	GCAAGGAGGA	AGAACTGGAA	GAAGTTCGGG	AACTCAGAGT	360
TTGACCCCCC	CGGACCCAAT	GTGGCCACCA	CCACTGTCAG	TGACGATGTC	TCTATGACGT	420
TCATCACCAG	CAAAGAGGAC	CTGAACTGCC	AGGAGGAGGA	GGACCCTATG	AACAAATTCA	480
AGGGCCAGAA	GATCGTGTCC	TGCCGCATCT	GCAAGGGCGA	CCACTGGACC	ACCCGCTGCC	540
CCTACAAGGA	TACGCTGGGG	CCCATGCAGA	AGGAGCTGGC	CGAGCAGCTG	GGCCTGTCTA	600
CTGGCGAGAA	GGAGAAGCTG	CCGGGAGAGC	TAGAGCCGGT	GCAGGCCACG	CAGAACAAGA	660
CAGGGAAGTA	TGTGCCGCCG	AGCCTGCGCG	ACGGGGCCAG	CCGCCGCGGG	GAGTCCATGC	720
AGCCCAACCG	CAGAGCCGAC	GACAACGCCA	CCATCCGTGT	CACCAACTTG	CGCAGAGGAC	780
ACGCGTGAGA	CCGACCTGCA	GGAGCTCTTC	CGGCCTTTTCG	GCTCCATCTC	CCGCATCTAC	840
CTGGCTAAGG	ACAAGACCAC	TGGCCAATCC	AAGGGCTTTG	CCTTCATCAG	CTTCCACCGC	900

CGCGAGGATG	CTGCGCGTGC	CATTGCCGGG	GTGTCCGGCT	TTGGCTACGA	CCACCTCATC	960
CTCAACGTCG	AGTGGGCCAA	GCCGTCCACC	AACTAAGCCA	GCTGCCACTG	TGTACTCGGT	1020
CCGGGACCCT	TGGCGACAGA	AGACAGCCTC	CGAGAGCGCG	GGCTCCAAGG	GCAATAAAGC	1080
AGCTCCACTC	TCAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1140
GC						1142

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCGGCA	CGAGGGAAAC	ATGGCGGTAG	GCTGGGACCA	TAACACAAGC	ATGACTATAT	60
GAAGGAAGAG	GAAGGTTTT	CTGAAGATGA	GGCGACTGAA	TCGGAAAAAA	ACTTTAAGTT	120
TGGTAAAAGA	GTTGGATGCC	TTTCCGAAGG	TTCCTGAGAG	CTATGTAGAG	ACTTCAGCCA	180
GTGGAGGTAC	AGTTTCTCTA	ATAGCATTTA	CAACTATGGC	TTTATTAACC	ATAATGGAAT	240
TCTCAGTATA	TCAAGATACA	TGGATGAAGT	ATGAATACGA	AGTAGACAAG	GATTTTTCTA	300
GCAAATTAAG	AATTAATATA	GATATTACTG	TTGCCATGAA	GTGTCAATAT	GTTGGAGCGG	360
ATGTATTGGA	TTTAGCAGAA	ACAATGGTTG	CATCTGCAGA	TGGTTTAGTT	TATGAACCAA	420
CAGTATTTGA	TCTTTCACCA	CAGCAGAAAG	AGTGGCAGAG	GATGCTGCAG	CTGATTCAGA	480
GTAGGCTACA	AGAAGAGCAT	TCACTTCAAG	ATGTGATATT	TAAAAGTGCT	TTTAAAAGTA	540
CATCAACAGC	TCTTCCACCA	AGAGAAGATG	ATTCATCACA	GTCTCCAAAT	GCATGCAGAA	600
TTCATGGCCA	TCTATATGTC	AATAAAGTAG	CAGGGAATTT	TCACATAACA	GTGGGCAAGG	660
CAATTCACCA	TCCTCGTGGT	CATGCACATT	TGGCAGCACT	TGTCAACCAT	GAATCTTACA	720
ATTTTTCTCA	TAGAATAGAT	CATTTGTCTT	TTGGAGAGCT	TGTTCCAGCA	ATTATTAATC	780
CTTTAGATGG	AACTGAAAA	ATTGCTATAG	ATCACAACCA	GATGTTCCAA	TATTTTATTA	840
CAGTTGTGCC	AACAAAATA	CATACATATA	AAATATCAGC	AGACACCCAT	CAGTTTTCTG	900
TGACAGAAAG	GGAACGTATC	ATTAACCATG	CTGCAGGCAG	CCATGGAGTC	TCTGGGATAT	960
TTATGAAATA	TGATCTCAGT	TCTCTTATGG	TGACAGTTAC	TGAGGAGCAC	ATGCCATTCT	1020
GGCAGTTTTT	TGTAAGACTC	TGTGGTATTG	TTGGAGGAAT	CTTTTCAACA	ACAGGCATGT	1080
TACATGGAAT	TGGAATAAT	ATAGTTGAAA	TAATTTGCTG	TCGTTTCAGA	CTTGGATCCT	1140
ATAAACCTGT	CAATTCTGTT	CCTTTTGAGG	ATGGCCACAC	AGACAACCAC	TTACCTCTTT	1200
TAGAAAATAA	TACACATTAA	CACCTCCCGA	TTGAAGGAGA	AAAACCTTTT	GCCTGAGACA	1260
TAAAACCTTT	TTTAAATAAT	AAAATATTGT	GCAATATATT	CAAAGAAAAG	AAAACACAAA	1320
TAAGCAGAAA	ACATACTTAT	TTTAAAAAAG	AAAAAAAAGG	ATAAAAAAAC	CCAAACTGAA	1380
ATTCTATATA	CGTTGTGTCT	GTTACAAATG	TCGTAGAAGA	AATCATGCAG	CTAAACGATG	1440
AAGAAGCCCA	ACTGGAGTGT	TGCTTTGAAG	ATGACGCCTT	CTTATATTTT	CATAGCAAAT	1500
GGGTGGTATC	AAAATCAGAC	ATTGCTTCTT	GCTGATAAAA	AGCCTGAAGG	AAATAAGTGA	1560
AACTACATCT	ATGGGAAAAA	AAAAAACATT	GAGAAGTGCA	AATGTTTCGA	TCCTTTTGTT	1620
TTTAAAGAT	ATGATGTCAG	AATAAAATGT	GGAAAACATA	CGGAAAAAAA	AAAAAAAATA	1680
AAATTCCTGC	GGCCGC					1696

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCGGCA	CGAGGCGGCA	CGAGGCGGCA	CGAGGGTGGC	ATATCACGGC	CATGGGGTCT	60
CAGCATTCGG	CTGCTGCTCG	CCCCTCCTCC	TGCAGGCGAA	AGCAAGAAGA	TGACAGGGAC	120
GGTTTGCTGG	CTGAACGAGA	GCAGGAAGAA	GCCATTGCTC	AGTTCCCATA	TGTGGAATTC	180
ACCGGGAGAG	ATAGCATCAC	CTGTCTCACG	TGCCAGGGGA	CAGGCTACAT	TCCAACAGAG	240
CAAGTAAATG	AGTTGGTGGC	TTTGATCCCA	CACAGTGATC	AGAGATTGCG	CCCTCAGCGA	300
ACTAAGCAAT	ATGTCCTCCT	GTCCATCCTG	CTTTGTCTCC	TGGCATCTGG	TTTGGTGGTT	360
TTCTTCCTGT	TTCCGCATTC	AGTCCTTGTG	GATGATGACG	GCATCAAAGT	GGTGAAAGTC	420
ACATTTAATA	AGCAAGACTC	CCTTGTAATT	CTCACCATCA	TGGCCACCCT	GAAAATCAGG	480
AACTCCAACT	TCTACACGGT	GGCAGTGACC	AGCCTGTCCA	GCCAGATTCA	GTACATGAAC	540
ACAGTGGTCA	GTACATATGT	GACTACTAAC	GTCTCCCTTA	TTCCACCTCG	GAGTGAGCAA	600
CTGGTGAATT	TTACCGGGAA	GGCCGAGATG	GGAGGACCGT	TTTCCTATGT	GTACTTCTTC	660
TGCACGGTAC	CTGAGATCCT	GGTGCACAAC	ATAGTGATCT	TCATGCGAAC	TTCAGTGAAG	720
ATTTCATACA	TTGGCCTCAT	GACCCAGAGC	TCCTTGGAGA	CACATCACTA	TGTGGATTGT	780
GGAGGAAATT	CCACAGCTAT	TTAACAACCTG	CTATTGGTTC	TTCCACACAG	CGCCTGTAGA	840
AGAGAGCACA	GCATATGTTC	CCAAGGCCTG	AGTTCTGGAC	CTACCCCCAC	GTGGTGTAAG	900
CAGAGGAGGA	ATTGGTTCAC	TTAACTCCCA	GCAAACATCC	TCCTGCCACT	TAGGAGGAAA	960
CACCTCCCTA	TGGTACCATT	TATGTTTCTC	AGAACCAGCA	GAATCAGTGC	CTAGCCTGTG	1020
CCCAGCAAAT	AGTTGGCACT	CAATAAAGAT	TTGCAGAATT	TAAAAAAAAA	AAAAAAAAAA	1080
AAAAAAATTC	CTGCGGCCGC					1100

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCGGCA	CGAGGGTACC	TGCTTTTCTA	TTGCCTCTTT	GAAACAATGG	TCACGTGTTT	60
CCATGTTCCC	TACTCGGCTC	TCACCATGTT	CATCAGCACC	GAGCAGACTG	AGCGGGATTC	120
TGCCACCGCC	TATCGGATGA	CTGTGGAAGT	GCTGGGCACA	GTGCTGGGCA	CGGCGATCCA	180
GGGACAAATC	GTGGGCCAAG	CAGACACGCC	TTGTTTCCAG	GACCTCAATA	GCTCTACAGT	240
AGCTTCACAA	AGTGCCAACC	ATACACATGG	CACCACCTCA	CACAGGGAAA	CGCAAAAGGC	300
ATACCTGCTG	GCAGCGGGGG	TCATTGTCTG	TATCTATATA	ATCTGTGCTG	TCATCCTGAT	360
CCTGGGCGTG	CGGGAGCAGA	GAGAACCCCTA	TGAAGCCCAG	CAGTCTGAGC	CAATCGCCTA	420
CTTCCGGGGC	CTACGGCTGG	TCATGAGCCA	CGGCCCATAC	ATCAAACCTTA	TTACTGGCTT	480
CCTCTTCACC	TCCTTGGCTT	TCATGCTGGT	GGAGGGGAAC	TTTGTCTTGT	TTTGCACCTA	540
CACCTTGGGC	TTCCGCAATG	AATTCCAGAA	TCTACTCCTG	GCCATCATGC	TCTCGGCCAC	600
TTTAACCATT	CCCATCTGGC	AGTGGTTCTT	GACCCGGTTT	GGCAAGAAGA	CAGCTGTATA	660
TGTTGGGATC	TCATCAGCAG	TGCCATTTCT	CATCTTGGTG	GCCCTCATGG	AGAGTAACCT	720
CATCATTACA	TATGCGGTAG	CTGTGGCAGC	TGGCATCAGT	GTGGCAGCTG	CCTTCTTACT	780
ACCCTGGTCC	ATGCTGCCTG	ATGTCATTGA	CGACTTCCAT	CTGAAGCAGC	CCCACTTCCA	840
TGGAACCGAG	CCCATCTTCT	TCTCCTTCTA	TGTCTTCTTC	ACCAAGTTTG	CCTCTGGAGT	900
GTCACCTGGC	ATTTCTACCC	TCAGTCTGGA	CTTTGCAGGG	TACCAGACCC	GTGGCTGCTC	960
GCAGCCGGAA	CGTGTCAAGT	TTAACTGAA	CATGCTCGTG	ACCATGGCTC	CCATAGTTCT	1020
CATCCTGCTG	GGCCTGCTGC	TCTTCAAAAT	GTACCCCAT	GATGAGGAGA	GGCGGCGGCA	1080
GAATAAGAAG	GCCCTGCAGG	CACTGAGGGA	CGAGGCCAGC	AGCTCTGGCT	GCTCAGAAAC	1140
AGACTCCACA	GAGCTGGCTA	GCATCCTCTA	GGGCCCCGCA	CGTTGCCCGA	AGCCACCATG	1200
CAGAAGGCCA	CAGAAGGGAT	CAGGACCTGT	CTGCCGGCTT	GCTGAGCAGC	TGGACTGCAG	1260
GTGCTAGGAA	GGGAAGTGA	GACTCAAGGA	GGTGGCCCAG	GACACTTGCT	GTGCTCACTG	1320
TGGGGCCGGC	TGCTCTGTGG	CCTCCTGCCT	CCCCTCTGCC	TGCCTGTGGG	GCCAAGCCCT	1380
GGGGCTGCCA	CTGTGAATAT	GCCAAGGACT	GATCGGGCCT	AGCCCGGAAC	ACTAATGTAG	1440
AAACCTTTTT	TTTACAGAGC	CTAATTAATA	ACTTAATGAC	TGTGTACATA	GCAATGTGTG	1500

TGTATGTATA TGTCTGTGAG CTATTAATGT TATTAATTTT CATAAAAGCT GGAAAGCAAA 1560
 AAAAAAAAAA AAAAATTCCT GCGGCCGC 1588

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA	CGAGGCGGAA	GTCCCGTCTC	ACGGTTGCCC	TGGCAGCGCG	CGAGGCTGGT	60
GAGTCGGCAG	CCCTGTGGCA	GCCGGCGGGC	TGGTTTCCAT	GGTTGCACGA	TTAGGAACCA	120
CCAGCTGCTG	CATCCCATGG	CCAGGGGTGG	CGTCCAGGTG	GCAGAGCAGC	TAGGAACGCA	180
AGGCCTGAAC	CTGGGGCCAG	ACACCCTGCT	CTCCCGGCCA	TGGTCAACGA	CCCTCCAGTA	240
CCTGCCTTAC	TGTGGGCCCA	GGAGGTGGGC	CAAGTCTTGG	CAGGCCGTGC	CCGCAGGCTG	300
CTGCTGCAGT	TTGGGGTGCT	CTTCTGCACC	ATCCTCCTTT	TGCTCTGGGT	GTCTGTCTTC	360
CTCTATGGCT	CCTTCTACTA	TTCTTATATG	CCGACAGTCA	GCCACCTCAG	CCCTGTGCAT	420
TTCTACTACA	GGACCGACTG	TGATTCCTCC	ACCACCTCAC	TCTGCTCCTT	CCCTGTTGCC	480
AATGTCTCGC	TGACTAAGGG	TGGACGTGAT	CGGGTGCTGA	TGTATGGACA	GCCGTATCGT	540
GTTACCTTAG	AGCTTGAGCT	GCCAGAGTCC	CCTGTGAATC	AAGATTTGGG	CATGTTCTTG	600
GTCACCATTT	CCTGCTACAC	CAGAGGTGGC	CGAATCATCT	CCACTTCTTC	GCGTTCGGTG	660
ATGCTGCATT	ACCGCTCAGA	CCTGCTCCAG	ATGCTGGACA	CACTGGTCTT	CTCTAGCCTC	720
CTGCTATTTG	GCTTTGCAGA	GCAGAAGCAG	CTGCTGGAGG	TGGAACTCTA	CGCAGACTAT	780
AGAGAGAACT	CGTACGTGCC	GACCACTGGA	GCGATCATTG	AGATCCACAG	CAAGCGCATC	840
CAGCTGTATG	GAGCCTACCT	CCGCATCCAC	GCGCACTTCA	CTGGGCTCAG	ATACCTGCTA	900
TACAACTTCC	CGATGACCTG	CGCCTTCATA	GGTGTTGCCA	GCAACTTCAC	CTTCCTCAGC	960
GTCATCGTGC	TCTTCAGCTA	CATGCAGTGG	GTGTGGGGGG	GCATCTGGCC	CCGACACCGC	1020
TTCTCTTTGC	AGGTTAACAT	CCGAAAAAGA	GACAATTCCC	GGAAGGAAGT	CCAACGAAGG	1080
ATCTCTGCTC	ATCAGCCAGG	GCCTGAAGGC	CAGGAGGAGT	CAACTCCGCA	ATCAGATGTT	1140
ACAGAGGATG	GTGAGAGCCC	TGAAGATCCC	TCAGGGACAG	AGGTCAGCTG	TCCGAGGAGG	1200
AGAAACCAGA	TCAGCAGCCC	CTGAGCGGAG	AAGAGGAGCT	AGAGCCTGAG	GCCAGTGATG	1260
G TTCAGGCTC	CTGGGAAGAT	GCAGCTTTGC	TGACGGAGGC	CAACCTGCCT	GCTCCTGCTC	1320
CTGCTTCTGC	TTCTGCCCCCT	GTCCTAGAGA	CTCTGGGCAG	CTCTGAACCT	GCTGGGGGTG	1380
CTCTCCGACA	GCGCCCCACC	TGCTCTAGTT	CCTGAAGAAA	AGGGGCAGAC	TCCTCACATT	1440
CCAGCACTTT	CCCACCTGAC	TCCTCTCCCC	TCGTTTTTCC	TTCAATAAAC	TATTTTGTGT	1500
CAAAAAAAAA	AAAAAAAAAA	AATTCCTGCG	GCCGC			1535

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCA	CGAGGGCGGG	CGCTACGGGC	TTGACTCCCC	CAAGGCCGAG	GTCCGCGGCC	60
AGGTGCTGGC	GCCGCTGCCC	CTCCACGGAG	TTGCTGATCA	TCTGGGCTGT	GATCCACAAA	120
CCCGGTTCTT	TGTCCCTCCT	AATATCAAAC	AGTGGATTGC	CTTGCTGCAG	AGGGGAAACT	180
GCACGTTTAA	AGAGAAAATA	TCACGGGCCG	CTTTCCACAA	TGCAGTTGCT	G TAGTCATCT	240
ACAATAATAA	ATCCAAAGAG	GAGCCAGTTA	CCATGACTCA	TCCAGGCACT	GGAGATATTA	300

TTGCTGTCAT	GATAACAGAA	TTGAGGGGTA	AGGATATTTT	GAGTTATCTG	GAGAAAAACA	360
TCTCTGTACA	AATGACAATA	GCTGTTGGAA	CTCGAATGCC	ACCGAAGAAC	TTCAGCCGTG	420
GCTCTCTAGT	CTTCGTGTCA	ATATCCTTTA	TTGTTTTGAT	GATTATTTCT	TCAGCATGGC	480
TCATATTCTA	CTTCATTCAA	AAGATCAGGT	ACACAAATGC	ACGCGACAGG	AACCAGCGTC	540
GTCTCGGAGA	TGCAGCCAAG	AAAGCCATCA	GTAAATTGAC	AACCAGGACA	GTAAAGAAGG	600
GTGACAAGGA	AACTGACCCA	GACTTTGATC	ATTGTGCAGT	CTGCATAGAG	AGCTATAAGC	660
AGAATGATGT	CGTCCGAATT	CTCCCCTGCA	AGCATGTTTT	CCACAAATCC	TGCGTGGATC	720
CCTGGCTTAG	TGAACATTGT	ACCTGTCCTA	TGTGCAAAC	TAATATATTG	AAGGCCCTGG	780
GAATTGTGCC	GAATTTGCCA	TGTACTGATA	ACGTAGCATT	CGATATGGAA	AGGCTCACCA	840
GAACCCAAGC	TGTAAACCGA	AGATCAGCCC	TCGGCGACCT	CGCCGGCGAC	AACTCCCTTG	900
GCCTTGAGCC	ACTTCGAAC	TCGGGGATCT	CACCTCTTCC	TCAGGATGGG	GAGCTCACTC	960
CGAGAACAGG	AGAAATCAAC	ATTGCAGTAA	CAAAAGAATG	GTTTATTATT	GCCAGTTTTG	1020
GCCTCCTCAG	TGCCCTCACA	CTCTGCTACA	TGATCATCAG	AGCCACAGCT	AGCTTGAATG	1080
CTAATGAGGT	AGAATGGTTT	TGAAGAAGAA	AAAACCTGCT	TTCTGACTGA	TTTTGCCTTG	1140
AAGGAAAAAA	GAACCTATTT	TTGTGCATCA	TTTACCAATC	ATGCCACACA	AGCATTTATT	1200
TTTAGTACAT	TTTATTTTTT	CATAAAATTG	CTAATGCCAA	AGCTTTGTAT	TAAAAGAAAT	1260
AAATAATAAA	ATAAAAAAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAT	TCCTGCGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCA	CGAGGCCCTC	CCGCGCTCCC	GGGGCGCGCG	GGCCGCGCCC	CCGACGCCCT	60
ACATATACTC	AGGTGCGCCC	CACCTGTCCG	CCCGCACCTG	CTGGCTCACC	TCCGAGCCAC	120
CTCTGCTGCG	CACCGCAGCC	TCGGACCTAC	AGCCAGGAT	ACTTTGGGAC	TTGCCGGCGC	180
TCAGAAACGC	GCCCAGACGG	CCCCTCCACC	TTTTGTTTGC	CTAGGGTCGC	CGAGAGCGCC	240
CGGAGGGAAC	CGCCTGGCCT	TCGGGGACCA	CCAATTTTGT	CTGGAACCAC	CCTCCCGGCG	300
TATCCTACTC	CCTGTGCCGC	GAGGCCATCG	CTTCACTGGA	GGGGTCGATT	TGTGTGTAGT	360
TTGGTGACAA	GATTTGCATT	CACCTGGCCC	AAACCTTTT	TGTCTCTTTG	GGTGACCGGA	420
AAACTCCACC	TCAAGTTTTC	TTTTGTGGGG	CTGCCCCCA	AGTGTCGTTT	GTTTTACTGT	480
AGGGTCTCCC	GCCCGGCGCC	CCCAGTGTTT	TCTGAGGGCG	GAAATGGCCA	ATTCGGGCCT	540
GCAGTTGCTG	GGCTTCTCCA	TGGCCCTGCT	GGGCTGGGTG	GGTCTGGTGG	CCTGCACCGC	600
CATCCCGCAG	TGGCAGATGA	GCTCCTATGC	GGGTGACAAC	ATCATCACGG	CCCAGGCCAT	660
GTACAAGGGG	CTGTGGATGG	ACTGCGTCAC	GCAGAGCACG	GGGATGATGA	GCTGCAAAAT	720
GTACGACTCG	GTGCTCGCCC	TGTCCGCGGC	CTTGCAGGCC	ACTCGAGCCC	TAATGGTGGT	780
CTCCCTGGTG	CTGGGCTTCC	TGGCCATGTT	TGTGGCCACG	ATGGGCATGA	AGTGCACGCG	840
CTGTGGGGGA	GACGACAAAG	TGAAGAAGGC	CCGTATAGCC	ATGGGTGGAG	GCATAATTTT	900
CATCGTGGCA	GGTCTTGCCG	CCTTGGTAGC	TTGCTCCTGG	TATGGCCATC	AGATTGTCAC	960
AGACTTTTAT	AACCTTTTGA	TCCCTACCAA	CATTAAGTAT	GAGTTTGGCC	CTGCCATCTT	1020
TATTGGCTGG	GCAGGGTCTG	CCCTAGTCAT	CCTGGGAGGT	GCACTGCTCT	CCTGTTCTCTG	1080
TCCTGGGAAT	GAGAGCAAGG	CTGGGTACCG	TGCACCCCGC	TCTTACCCTA	AGTCCAATCTC	1140
TTCCAAGGAG	TATGTGTGAC	CTGGGATCTC	CTTGCCCCAG	CCTGACAGGC	TATGGGAGTG	1200
TCTAGATGCC	TGAAAGGGCC	TGGGGCTGAG	CTCAGCCTGT	GGGCAGGGTG	CCGGACAAAG	1260
GCCTCCTGGT	CACTCTGTCC	CTGCACTCCA	TGTATAGTCC	TCTTGGGTTG	GGGGTGGGGG	1320
GGTGCCGTTG	GTGGGAGAGA	CAAAAAGAGG	GAGAGTGTGC	TTTTTGTACA	GTAATAAAAA	1380
ATAAGTATTG	GGAAGCAGGC	TTTTTTCCCT	TCAGGGCCTC	TGCTTTCCTC	CCGTCCAGAT	1440
CCTTGCAGGG	AGCTTGGAAC	CTTAGTGCAC	CTACTTCAGT	TCAGAACACT	TAGCACCCCA	1500
CTGACTCCAC	TGACAATTGA	CTAAAAGATG	CAGGTGCTCG	TATCTCGACA	TTCATTTCCA	1560
CCCCCTCTT	ATTAAATAG	CTACCAAAGT	ACTTCTTTTT	TAATAAAAAA	ATAAAGATTT	1620

TTATTAGGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680
 AAAAAAAAAA AAAAAAATT CCTGCGGCCG C 1711

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGCA	CGAGGGCAGG	TCCAGAGTAA	AGTCACTGAA	GAGTGGAAGC	GAGGAAGGAA	60
CAGGATGATT	AGACCTCAGC	TGCGGACCGC	GGGGCTGGGA	CGATGCCTCC	TGCCGGGGCT	120
GCTGCTGCTC	CTGGTGCCCG	TCCTCTGGGC	CGGGGCTGAA	AAGCTACATA	CCCAGCCCTC	180
CTGCCCCGCG	GTCTGCCAGC	CCACGCGCTG	CCCCGCGCTG	CCCACCTGCG	CGCTGGGGAC	240
CACGCCGGTG	TTCGACCTGT	GCCGCTGTTG	CCGCGTCTGC	CCCGCGGCCG	AGCGTGAAGT	300
CTGCGGCGGG	GCGCAGGGCC	AACCGTGCGC	CCCGGGGCTG	CAGTGCCTCC	AGCCGCTGCG	360
CCCCGGGTTC	CCCAGCACCT	GCGGTTGCCC	GACGCTGGGA	GGGGCCGTGT	GCGGCAGCGA	420
CAGGCGCACC	TACCCAGCA	TGTGCGCGCT	CCGGGCCGAA	AACCGCGCCG	CGCGCCGCCT	480
GGGCAAGGTC	CCGGCCGTGC	CTGTGCAGTG	GGGGAAGTGC	GGGGATACAG	GGACCAGAAG	540
CGCAGGCCCG	CTCAGGAGGA	ATTACAACTT	CATCGCCGCG	GTGGTGGAGA	AGGTGGCGCC	600
ATCGGTGGTT	CACGTGCAGC	TGTGGGGCAG	GTTACTTCAC	GGCAGCAGGC	TTGTTCTCTG	660
GTACAGTGGC	TCTGGGTTCA	TAGTGTCTGA	GGACGGGCTC	ATTATTACCA	ATGCCCATGT	720
TGTCAGGAAC	CAGCAGTGGA	TTGAGGTGGT	GCTCCAGAAT	GGGGCCCGTT	ATGAAGCTGT	780
TGTCAAGGAT	ATTGACCTTA	AATTGGATCT	TGCGGTGATT	AAGATTGAAT	CAAATGCTGA	840
ACTTCCTGTA	CTGATGCTGG	GAAGATCATC	TGACCTTCGG	GCTGGAGAGT	TTGTGGTGGC	900
TTTGGGCAGC	CCATTTTCTC	TGCAGAACAC	AGCTACTGCA	GGAATTGTCA	GCACCAAACA	960
GCGAGGGGGC	AAAGAACTGG	GGATGAAGGA	TTCAGATATG	GACTACGTCC	AGATTGATGC	1020
CACAATTAAC	TATGGGAATT	CTGGTGGTCC	TCTGGTGAAC	TTGGATGGTG	ATGTGATTGG	1080
CGTCAATTCA	TTGAGGGTGA	CTGATGGAAT	CTCCTTTGCA	ATTCTTCAG	ATCGAGTTAG	1140
GCAGTTCTTG	GCAGAATACC	ATGAGCACCA	GATGAAAGGA	AAGGCGTTTT	CAAATAAGAA	1200
ATATCTGGGT	CTGCAAATGC	TGTCCCTCAC	TGTGCCCTT	AGTGAAGAAT	TGAAAATGCA	1260
TTATCCAGAT	TTCCCTGATG	TGAGTTCTGG	GGTTTATGTA	TGTAAAGTGG	TTGAAGGAAC	1320
AGCTGCTCAA	AGCTCTGGAT	TGAGAGATCA	CGATGTAATT	GTCAACATAA	ATGGGAAACC	1380
TATTACTACT	ACAACCTGAT	TTGTTAAAGC	TCTTGACAGT	GATTCCCTTT	CCATGGCTGT	1440
TCTTCGGGGA	AAAGATAATT	TGCTCCTGAC	AGTCATACCT	GAAACAATCA	ATTAAATATC	1500
TTGTTTTAAA	GTGGGATTAT	CTAAAAAATA	AAAAAATAAA	TTCCTGCGGC	CGC	1553

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA	CGAGGGGAGC	CGCTCCCCGA	GCCCCGGCCGT	AGAGGCTGCA	ATCGCAGCCG	60
GGAGCCCGCA	GCCCCGCGCC	CGAGCCCGCC	GCCGCCCTTC	GAGGGCGCCC	CAGGCCGCGC	120
CATGGTGAAG	GTGACGTTCA	ACTCCGCTCT	GGCCCAGAAG	GAGGCCAAGA	AGGACGAGCC	180
CGAGAGCGGC	GAGGAGGCGC	TCATCATCCC	CCCCGACGCC	GTCGCGGTGG	ACTGCAAGGA	240


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CCCAGATGAT GTGGTACCAG TTGGCCAAAG AAGAGCCTGG TGTGCTTTGG 300
ACTAGCATTT ATGCTTGCAG GTGTTATTCT AGGAGGAGCA TACTTGTACA AATATTTTGC 360
ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT 420
AAATGAGCCC TCTGCAGATG CCCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA 480
AATCTTTGAA GAAGAAGAAG TTGAATTTAT CAGTGTGCCT GTCCCAGAGT TTGCAGATAG 540
TGATCCTGCC AACATTGTTC ATGACTTTAA CAAGAACTT ACAGCCTATT TAGATCTTAA 600
CCTGGATAAG TGCTATGTGA TCCCTCTGAA CACTTCCATT GTTATGCCAC CCAGAAACCT 660
ACTGGAGTTA CTTATTAACA TCAAGGCTGG AACCTATTTG CCTCAGTCCT ATCTGATTCA 720
TGAGCACATG GTTATTACTG ATCGCATTGA AAACATTGAT CACCTGGGTT TCTTTATTTA 780
TCGACTGTGT CATGACAAGG AAACCTACAA ACTGCAACGC AGAGAACTA TTAAAGGTAT 840
TCAGAAACGT GAAGCCAGCA ATTGTTTCGC AATTCGGCAT TTTGAAAACA AATTGCCGT 900
GGAAACTTTA ATTTGTTCTT GAACAGTCAA GAAAAACATT ATTGAGGAAA ATTAATATCA 960
CAGCATAACC CCACCCTTTA CATTTTGTGC AGTGATATTT TTTAAAGTCT CTTTCATGTA 1020
AGTAGCAAAC AGGGCTTTAC TATCTTTTCA TCTCATTAAT TCAATTAAAA CCATTACCTT 1080
AAAATTTTTT TCTTTCGAAG TGTGGTGTCT TTTATATTTG AATTAGTAAC TGTATGAAGT 1140
CATAGATAAT AGTACATGTC ACCTTAGGTA GTAGGAAGAA TTACAATTTT TTTAAATCAT 1200
TTATCTGGAT TTTTATGTTT TATTAGCATT TTCAAGAAGA CGGATTATCT AGAGAATAAT 1260
CATATATATG CACATGTAAC AATGGACCAC AGTGACTTAT TTGTAGTTGT TAGTTGCCCT 1320
GCTACCTAGT TTGTTAGTGC ATTTGAGCAC ACATTTTAAT TTTCTCTAA TTTAAATGTG 1380
CAGTATTTTC AGTGTCAAAT ATATTAACT ATTTAGAGAA TGATTTCCAC CTTTATGTTT 1440
TAATATCCTA GGCATCTGCT GTAATAATAT TTTAGAAAAT GTTTGAATT TAAGAAATAA 1500
CTTGTGTTAC TAATTTGTAT AACCCATATC TGTGCAATGG AATATAAATA TCACAAAGTT 1560
GTTTAAAAAA AAAAAAAAAA AAATTCCTGC GGCCGC 1596

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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Met Ala Trp Arg Arg Arg Glu Ala Gly Val Gly Ala Arg Gly Val Leu
 1           5           10           15
Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly
 20           25           30
Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp
 35           40           45
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe
 50           55           60
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro
 65           70           75           80
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe
 85           90           95
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu
100          105          110
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala
115          120          125
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly
130          135          140
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val
145          150          155          160
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln

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				165					170					175					
Lys	Gly	Ile	Pro	Val	Thr	Met	Thr	Ile	Gly	Val	Gly	Thr	Arg	His	Val				
			180					185					190						
Gln	Glu	Phe	Ile	Ser	Gly	Gln	Ser	Val	Val	Phe	Val	Ala	Ile	Ala	Phe				
		195					200					205							
Ile	Thr	Met	Met	Ile	Ile	Ser	Leu	Ala	Trp	Leu	Ile	Phe	Tyr	Tyr	Ile				
	210					215					220								
Gln	Arg	Phe	Leu	Tyr	Thr	Gly	Ser	Gln	Ile	Gly	Ser	Gln	Ser	His	Arg				
225					230					235					240				
Lys	Glu	Thr	Lys	Lys	Val	Ile	Gly	Gln	Leu	Leu	Leu	His	Thr	Val	Lys				
			245					250				255							
His	Gly	Glu	Lys	Gly	Ile	Asp	Val	Asp	Ala	Glu	Asn	Cys	Ala	Val	Cys				
		260				265						270							
Ile	Glu	Asn	Phe	Lys	Val	Lys	Asp	Ile	Ile	Arg	Ile	Leu	Pro	Cys	Lys				
	275					280						285							
His	Ile	Phe	His	Arg	Ile	Cys	Ile	Asp	Pro	Trp	Leu	Leu	Asp	His	Arg				
	290				295						300								
Thr	Cys	Pro	Met	Cys	Lys	Leu	Asp	Val	Ile	Lys	Ala	Leu	Gly	Tyr	Trp				
305					310					315					320				
Gly	Glu	Pro	Gly	Asp	Val	Gln	Glu	Met	Pro	Ala	Pro	Glu	Ser	Pro	Pro				
			325					330				335							
Gly	Arg	Asp	Pro	Ala	Ala	Asn	Leu	Ser	Leu	Ala	Leu	Pro	Asp	Asp	Asp				
		340				345						350							
Gly	Ser	Asp	Asp	Ser	Ser	Pro	Pro	Ser	Ala	Ser	Pro	Ala	Glu	Ser	Glu				
	355					360					365								
Pro	Gln	Cys	Asp	Pro	Ser	Phe	Lys	Gly	Asp	Ala	Gly	Glu	Asn	Thr	Ala				
	370				375						380								
Leu	Leu	Glu	Ala	Gly	Arg	Ser	Asp	Ser	Arg	His	Gly	Gly	Pro	Ile	Ser				
385				390				395							400				

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Asp	Lys	Gly	Ser	Ala	Gly	His	Pro	Gly	Gly	Val	Leu	Val	Trp	Gly				
1				5				10						15					
Arg	Ser	Pro	Ala	Pro	Thr	Ala	Leu	Trp	Gly	Ala	Ser	Pro	Trp	Leu	Ser				
		20					25						30						
Pro	Leu	Thr	Ser	Ala	Leu	Arg	Gln	Pro	Leu	His	Arg	Ala	Pro	Leu	Leu				
	35					40						45							
Pro	Gly	Gln	Leu	Cys	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Lys	Asn	Lys	Ala				
	50			55				60											
Met	Gly	Arg	Pro	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Gln	Pro	Pro					
65				70				75						80					
Ala	Phe	Leu	Gln	Pro	Gly	Gly	Ser	Thr	Gly	Ser	Gly	Pro	Ser	Tyr	Leu				
			85					90						95					
Tyr	Gly	Val	Thr	Gln	Pro	Lys	His	Leu	Ser	Ala	Ser	Met	Gly	Gly	Ser				
		100						105					110						
Val	Glu	Ile	Pro	Phe	Ser	Phe	Tyr	Tyr	Pro	Trp	Glu	Leu	Ala	Ile	Val				

[illegible][illegible][illegible]

- [illegible]

[illegible][illegible]

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

				165					170					175			
Val	Val	Val	His	Ala	Cys	Arg	Asn	Leu	Ile	Ala	Phe	Ser	Glu	Asp	Gly		
			180					185					190				
Ser	Asp	Pro	Tyr	Val	Arg	Met	Tyr	Leu	Leu	Pro	Asp	Lys	Arg	Arg	Ser		
		195					200					205					
Gly	Arg	Arg	Lys	Thr	His	Val	Ser	Lys	Lys	Thr	Leu	Asn	Pro	Val	Phe		
	210					215					220						
Asp	Gln	Ser	Phe	Asp	Phe	Ser	Val	Ser	Leu	Pro	Glu	Val	Gln	Arg	Arg		
225					230					235					240		
Thr	Leu	Asp	Val	Ala	Val	Lys	Asn	Ser	Gly	Gly	Phe	Leu	Ser	Lys	Asp		
				245					250					255			
Lys	Gly	Leu	Leu	Gly	Lys	Val	Leu	Val	Ala	Leu	Ala	Ser	Glu	Glu	Leu		
			260					265					270				
Ala	Lys	Gly	Trp	Thr	Gln	Trp	Tyr	Asp	Leu	Thr	Glu	Asp	Gly	Thr	Arg		
		275					280					285					
Pro	Gln	Ala	Met	Thr													
		290															

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Glu	Arg	Arg	His	Pro	Val	Cys	Ser	Gly	Thr	Cys	Gln	Pro	Thr	Gln		
1				5					10					15			
Phe	Arg	Cys	Ser	Asn	Gly	Cys	Cys	Ile	Asp	Ser	Phe	Leu	Glu	Cys	Asp		
			20					25					30				
Asp	Thr	Pro	Asn	Cys	Pro	Asp	Ala	Ser	Asp	Glu	Ala	Ala	Cys	Glu	Lys		
		35					40					45					
Tyr	Thr	Ser	Gly	Phe	Asp	Glu	Leu	Gln	Arg	Ile	His	Phe	Pro	Ser	Asp		
	50				55					60							
Lys	Gly	His	Cys	Val	Asp	Leu	Pro	Asp	Thr	Gly	Leu	Cys	Lys	Glu	Ser		
65					70				75					80			
Ile	Pro	Arg	Trp	Tyr	Tyr	Asn	Pro	Phe	Ser	Glu	His	Cys	Ala	Arg	Phe		
			85					90					95				
Thr	Tyr	Gly	Gly	Cys	Tyr	Gly	Asn	Lys	Asn	Asn	Phe	Glu	Glu	Glu	Gln		
			100					105					110				
Gln	Cys	Leu	Glu	Ser	Cys	Arg	Gly	Ile	Ser	Lys	Lys	Asp	Val	Phe	Gly		
	115						120					125					
Leu	Arg	Arg	Glu	Ile	Pro	Ile	Pro	Ser	Thr	Gly	Ser	Val	Glu	Met	Ala		
	130					135					140						
Val	Ala	Val	Phe	Leu	Val	Ile	Cys	Ile	Val	Val	Val	Val	Ala	Ile	Leu		
145					150					155					160		
Gly	Tyr	Cys	Phe	Phe	Lys	Asn	Gln	Arg	Lys	Asp	Phe	His	Gly	His	His		
			165						170				175				
His	His	Pro	Pro	Pro	Thr	Pro	Ala	Ser	Ser	Thr	Val	Ser	Thr	Thr	Glu		
		180						185					190				
Asp	Thr	Glu	His	Leu	Val	Tyr	Asn	His	Thr	Thr	Arg	Pro	Leu				
		195					200					205					

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

1

NAME	ADDRESS	CITY	STATE	ZIP
Mr. J. H. Smith	123 Main St.	Springfield	Ill.	62761
Mr. W. R. Jones	456 Oak Ave.	Chicago	Ill.	60601
Mr. T. L. Brown	789 Elm St.	Peoria	Ill.	61601
Mr. S. K. White	101 Maple Dr.	Rockford	Ill.	61101
Mr. M. N. Black	202 Pine St.	Decatur	Ill.	62521
Mr. P. Q. Green	303 Cedar Ave.	Normal	Ill.	62451
Mr. R. S. Hall	404 Birch St.	Urbana	Ill.	61501
Mr. V. T. King	505 Walnut Dr.	Champaign	Ill.	61821
Mr. Y. U. Lee	606 Spruce St.	Carbondale	Ill.	62901
Mr. Z. V. Scott	707 Ash Ave.	Macomb	Ill.	61451
Mr. A. W. Adams	808 Hickory St.	Edwardsville	Ill.	62021
Mr. B. X. Baker	909 Willow Dr.	St. Louis	Mo.	63101
Mr. C. Y. Carter	1010 Cherry St.	St. Paul	Mn.	55101
Mr. D. Z. Davis	1111 Elm St.	Minneapolis	Mn.	55401
Mr. E. A. Evans	1212 Oak Ave.	Portland	Me.	04101
Mr. F. B. Foster	1313 Pine St.	Boston	Ma.	02101
Mr. G. C. Gibson	1414 Maple Dr.	New York	Ny.	10001
Mr. H. D. Hall	1515 Birch St.	Los Angeles	Ca.	90001
Mr. I. E. Hill	1616 Walnut Dr.	Hollywood	Ca.	90021
Mr. J. F. Hill	1717 Spruce St.	San Francisco	Ca.	94101
Mr. K. G. Hill	1818 Ash Ave.	San Diego	Ca.	92101
Mr. L. H. Hill	1919 Hickory St.	San Jose	Ca.	95101
Mr. M. I. Hill	2020 Willow Dr.	San Antonio	Tx.	78101
Mr. N. J. Hill	2121 Cherry St.	Austin	Tx.	78701
Mr. O. K. Hill	2222 Elm St.	Dallas	Tx.	75201
Mr. P. L. Hill	2323 Oak Ave.	Fort Worth	Tx.	76101
Mr. Q. M. Hill	2424 Pine St.	Phoenix	Az.	85001
Mr. R. N. Hill	2525 Maple Dr.	Tucson	Az.	85701
Mr. S. O. Hill	2626 Birch St.	Albuquerque	Nm.	87101
Mr. T. P. Hill	2727 Walnut Dr.	Las Vegas	Nv.	89101
Mr. U. Q. Hill	2828 Spruce St.	Las Vegas	Nv.	89101
Mr. V. R. Hill	2929 Ash Ave.	Las Vegas	Nv.	89101
Mr. W. S. Hill	3030 Hickory St.	Las Vegas	Nv.	89101
Mr. X. T. Hill	3131 Willow Dr.	Las Vegas	Nv.	89101
Mr. Y. U. Hill	3232 Cherry St.	Las Vegas	Nv.	89101
Mr. Z. V. Hill	3333 Elm St.	Las Vegas	Nv.	89101
Mr. A. W. Hill	3434 Oak Ave.	Las Vegas	Nv.	89101
Mr. B. X. Hill	3535 Pine St.	Las Vegas	Nv.	89101
Mr. C. Y. Hill	3636 Maple Dr.	Las Vegas	Nv.	89101
Mr. D. Z. Hill	3737 Birch St.	Las Vegas	Nv.	89101
Mr. E. A. Hill	3838 Walnut Dr.	Las Vegas	Nv.	89101
Mr. F. B. Hill	3939 Spruce St.	Las Vegas	Nv.	89101
Mr. G. C. Hill	4040 Ash Ave.	Las Vegas	Nv.	89101
Mr. H. D. Hill	4141 Hickory St.	Las Vegas	Nv.	89101
Mr. I. E. Hill	4242 Willow Dr.	Las Vegas	Nv.	89101
Mr. J. F. Hill	4343 Cherry St.	Las Vegas	Nv.	89101
Mr. K. G. Hill	4444 Elm St.	Las Vegas	Nv.	89101
Mr. L. H. Hill	4545 Oak Ave.	Las Vegas	Nv.	89101
Mr. M. I. Hill	4646 Pine St.	Las Vegas	Nv.	89101
Mr. N. J. Hill	4747 Maple Dr.	Las Vegas	Nv.	89101
Mr. O. K. Hill	4848 Birch St.	Las Vegas	Nv.	89101
Mr. P. L. Hill	4949 Walnut Dr.	Las Vegas	Nv.	89101
Mr. Q. M. Hill	5050 Spruce St.	Las Vegas	Nv.	89101
Mr. R. N. Hill	5151 Ash Ave.	Las Vegas	Nv.	89101
Mr. S. O. Hill	5252 Hickory St.	Las Vegas	Nv.	89101
Mr. T. P. Hill	5353 Willow Dr.	Las Vegas	Nv.	89101
Mr. U. Q. Hill	5454 Cherry St.	Las Vegas	Nv.	89101
Mr. V. R. Hill	5555 Elm St.	Las Vegas	Nv.	89101
Mr. W. S. Hill	5656 Oak Ave.	Las Vegas	Nv.	89101
Mr. X. T. Hill	5757 Pine St.	Las Vegas	Nv.	89101
Mr. Y. U. Hill	5858 Maple Dr.	Las Vegas	Nv.	89101
Mr. Z. V. Hill	5959 Birch St.	Las Vegas	Nv.	89101
Mr. A. W. Hill	6060 Walnut Dr.	Las Vegas	Nv.	89101
Mr. B. X. Hill	6161 Spruce St.	Las Vegas	Nv.	89101
Mr. C. Y. Hill	6262 Ash Ave.	Las Vegas	Nv.	89101
Mr. D. Z. Hill	6363 Hickory St.	Las Vegas	Nv.	89101
Mr. E. A. Hill	6464 Willow Dr.	Las Vegas	Nv.	89101
Mr. F. B. Hill	6565 Cherry St.	Las Vegas	Nv.	89101
Mr. G. C. Hill	6666 Elm St.	Las Vegas	Nv.	89101
Mr. H. D. Hill	6767 Oak Ave.	Las Vegas	Nv.	

NAME	ADDRESS	CITY	STATE	ZIP
Mr. J. H. Smith	123 Main St.	Springfield	Ill.	62761
Mr. W. R. Jones	456 Oak Ave.	Chicago	Ill.	60601
Mr. T. L. Brown	789 Elm St.	Peoria	Ill.	61601
Mr. S. K. White	101 Maple Dr.	Rockford	Ill.	61101
Mr. M. D. Green	202 Pine St.	Decatur	Ill.	62521
Mr. L. P. Black	303 Cedar Ave.	Normal	Ill.	62451
Mr. N. Q. Gray	404 Birch St.	Urbana	Ill.	61501
Mr. R. S. Hall	505 Walnut Dr.	Champaign	Ill.	61821
Mr. P. T. King	606 Spruce Ave.	Carbondale	Ill.	62901
Mr. Q. U. Lee	707 Fir St.	Macomb	Ill.	61451
Mr. V. W. Scott	808 Ash Dr.	Edwardsville	Ill.	62021
Mr. X. Y. Adams	909 Hickory Ave.	St. Louis	Mo.	63101
Mr. Z. A. Baker	1010 Sycamore St.	St. Charles	Mo.	63071
Mr. B. C. Clark	1111 Chestnut Dr.	St. Joseph	Mo.	64501
Mr. D. E. Evans	1212 Locust Ave.	St. Louis	Mo.	63101
Mr. F. G. Harris	1313 Olive St.	St. Louis	Mo.	63101
Mr. H. I. Jackson	1414 Poplar Dr.	St. Louis	Mo.	63101
Mr. J. K. Lewis	1515 Birch Ave.	St. Louis	Mo.	63101
Mr. L. M. Miller	1616 Cedar St.	St. Louis	Mo.	63101
Mr. N. O. Wilson	1717 Elm Dr.	St. Louis	Mo.	63101
Mr. P. Q. Young	1818 Maple Ave.	St. Louis	Mo.	63101
Mr. R. S. Green	1919 Pine St.	St. Louis	Mo.	63101
Mr. T. U. White	2020 Oak Dr.	St. Louis	Mo.	63101
Mr. V. W. Black	2121 Elm Ave.	St. Louis	Mo.	63101
Mr. X. Y. Gray	2222 Birch St.	St. Louis	Mo.	63101
Mr. Z. A. Hall	2323 Cedar Dr.	St. Louis	Mo.	63101
Mr. B. C. King	2424 Elm Ave.	St. Louis	Mo.	63101
Mr. D. E. Lee	2525 Maple St.	St. Louis	Mo.	63101
Mr. F. G. Scott	2626 Pine Dr.	St. Louis	Mo.	63101
Mr. H. I. Adams	2727 Oak Ave.	St. Louis	Mo.	63101
Mr. J. K. Baker	2828 Elm St.	St. Louis	Mo.	63101
Mr. L. M. Clark	2929 Maple Dr.	St. Louis	Mo.	63101
Mr. N. O. Evans	3030 Pine Ave.	St. Louis	Mo.	63101
Mr. P. Q. Harris	3131 Oak St.	St. Louis	Mo.	63101
Mr. R. S. Jackson	3232 Elm Dr.	St. Louis	Mo.	63101
Mr. T. U. Lewis	3333 Maple Ave.	St. Louis	Mo.	63101
Mr. V. W. Miller	3434 Pine St.	St. Louis	Mo.	63101
Mr. X. Y. Wilson	3535 Oak Dr.	St. Louis	Mo.	63101
Mr. Z. A. Young	3636 Elm Ave.	St. Louis	Mo.	63101
Mr. B. C. Green	3737 Maple St.	St. Louis	Mo.	63101
Mr. D. E. White	3838 Pine Dr.	St. Louis	Mo.	63101
Mr. F. G. Black	3939 Oak Ave.	St. Louis	Mo.	63101
Mr. H. I. Gray	4040 Elm St.	St. Louis	Mo.	63101
Mr. J. K. Hall	4141 Maple Dr.	St. Louis	Mo.	63101
Mr. L. M. King	4242 Pine Ave.	St. Louis	Mo.	63101
Mr. N. O. Lee	4343 Oak St.	St. Louis	Mo.	63101
Mr. P. Q. Scott	4444 Elm Dr.	St. Louis	Mo.	63101
Mr. R. S. Adams	4545 Maple Ave.	St. Louis	Mo.	63101
Mr. T. U. Baker	4646 Pine St.	St. Louis	Mo.	63101
Mr. V. W. Clark	4747 Oak Dr.	St. Louis	Mo.	63101
Mr. X. Y. Evans	4848 Elm Ave.	St. Louis	Mo.	63101
Mr. Z. A. Harris	4949 Maple St.	St. Louis	Mo.	63101
Mr. B. C. Jackson	5050 Pine Dr.	St. Louis	Mo.	63101
Mr. D. E. Lewis	5151 Oak Ave.	St. Louis	Mo.	63101
Mr. F. G. Miller	5252 Elm St.	St. Louis	Mo.	63101
Mr. H. I. Wilson	5353 Maple Dr.	St. Louis	Mo.	63101
Mr. J. K. Young	5454 Pine Ave.	St. Louis	Mo.	63101
Mr. L. M. Green	5555 Oak St.	St. Louis	Mo.	63101
Mr. N. O. White	5656 Elm Dr.	St. Louis	Mo.	63101
Mr. P. Q. Black	5757 Maple Ave.	St. Louis	Mo.	63101
Mr. R. S. Gray	5858 Pine St.	St. Louis	Mo.	63101
Mr. T. U. Hall	5959 Oak Dr.	St. Louis	Mo.	63101
Mr. V. W. King	6060 Elm Ave.	St. Louis	Mo.	63101
Mr. X. Y. Lee	6161 Maple St.	St. Louis	Mo.	63101
Mr. Z. A. Scott	6262 Pine Dr.	St. Louis	Mo.	63101
Mr. B. C. Adams	6363 Oak Ave.	St. Louis	Mo.	63101
Mr. D. E. Baker	6464 Elm St.	St. Louis	Mo.	63101
Mr. F. G. Clark	6565 Maple Dr.	St. Louis	Mo.	63101
Mr. H. I. Evans	6666 Pine Ave.	St. Louis	Mo.	

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Mr. S. K. White	101 Maple Dr.	Rockford	Ill.	61101
Mr. M. N. Black	202 Pine St.	Decatur	Ill.	62521
Mr. P. Q. Green	303 Cedar Ave.	Normal	Ill.	62451
Mr. R. S. Hall	404 Birch St.	Urbana	Ill.	61501
Mr. V. T. King	505 Walnut Dr.	Champaign	Ill.	61821
Mr. Y. U. Lee	606 Spruce St.	Carbondale	Ill.	62901
Mr. Z. V. Scott	707 Ash Ave.	Macomb	Ill.	61451
Mr. A. W. Adams	808 Hickory St.	Edwardsville	Ill.	62021
Mr. B. X. Baker	909 Willow Dr.	St. Louis	Mo.	63101
Mr. C. Y. Carter	1010 Cherry St.	St. Paul	Mn.	55101
Mr. D. Z. Davis	1111 Elm St.	Minneapolis	Mn.	55401
Mr. E. A. Evans	1212 Oak Ave.	Portland	Me.	04101
Mr. F. B. Foster	1313 Pine St.	Boston	Ma.	02101
Mr. G. C. Gibson	1414 Maple Dr.	New York	Ny.	10001
Mr. H. D. Hall	1515 Birch St.	Los Angeles	Ca.	90001
Mr. I. E. Hill	1616 Walnut Dr.	Hollywood	Ca.	90021
Mr. J. F. Hill	1717 Spruce St.	San Francisco	Ca.	94101
Mr. K. G. Hill	1818 Ash Ave.	San Diego	Ca.	92101
Mr. L. H. Hill	1919 Hickory St.	San Jose	Ca.	95101
Mr. M. I. Hill	2020 Willow Dr.	San Antonio	Tx.	78101
Mr. N. J. Hill	2121 Cherry St.	Austin	Tx.	78701
Mr. O. K. Hill	2222 Elm St.	Dallas	Tx.	75201
Mr. P. L. Hill	2323 Oak Ave.	Fort Worth	Tx.	76101
Mr. Q. M. Hill	2424 Pine St.	Phoenix	Az.	85001
Mr. R. N. Hill	2525 Maple Dr.	Tucson	Az.	85701
Mr. S. O. Hill	2626 Birch St.	Albuquerque	Nm.	87101
Mr. T. P. Hill	2727 Walnut Dr.	Las Vegas	Nv.	89101
Mr. U. Q. Hill	2828 Spruce St.	Las Vegas	Nv.	89101
Mr. V. R. Hill	2929 Ash Ave.	Las Vegas	Nv.	89101
Mr. W. S. Hill	3030 Hickory St.	Las Vegas	Nv.	89101
Mr. X. T. Hill	3131 Willow Dr.	Las Vegas	Nv.	89101
Mr. Y. U. Hill	3232 Cherry St.	Las Vegas	Nv.	89101
Mr. Z. V. Hill	3333 Elm St.	Las Vegas	Nv.	89101
Mr. A. W. Hill	3434 Oak Ave.	Las Vegas	Nv.	89101
Mr. B. X. Hill	3535 Pine St.	Las Vegas	Nv.	89101
Mr. C. Y. Hill	3636 Maple Dr.	Las Vegas	Nv.	89101
Mr. D. Z. Hill	3737 Birch St.	Las Vegas	Nv.	89101
Mr. E. A. Hill	3838 Walnut Dr.	Las Vegas	Nv.	89101
Mr. F. B. Hill	3939 Spruce St.	Las Vegas	Nv.	89101
Mr. G. C. Hill	4040 Ash Ave.	Las Vegas	Nv.	89101
Mr. H. D. Hill	4141 Hickory St.	Las Vegas	Nv.	89101
Mr. I. E. Hill	4242 Willow Dr.	Las Vegas	Nv.	89101
Mr. J. F. Hill	4343 Cherry St.	Las Vegas	Nv.	89101
Mr. K. G. Hill	4444 Elm St.	Las Vegas	Nv.	89101
Mr. L. H. Hill	4545 Oak Ave.	Las Vegas	Nv.	89101
Mr. M. I. Hill	4646 Pine St.	Las Vegas	Nv.	89101
Mr. N. J. Hill	4747 Maple Dr.	Las Vegas	Nv.	89101
Mr. O. K. Hill	4848 Birch St.	Las Vegas	Nv.	89101
Mr. P. L. Hill	4949 Walnut Dr.	Las Vegas	Nv.	89101
Mr. Q. M. Hill	5050 Spruce St.	Las Vegas	Nv.	89101
Mr. R. N. Hill	5151 Ash Ave.	Las Vegas	Nv.	89101
Mr. S. O. Hill	5252 Hickory St.	Las Vegas	Nv.	89101
Mr. T. P. Hill	5353 Willow Dr.	Las Vegas	Nv.	89101
Mr. U. Q. Hill	5454 Cherry St.	Las Vegas	Nv.	89101
Mr. V. R. Hill	5555 Elm St.	Las Vegas	Nv.	89101
Mr. W. S. Hill	5656 Oak Ave.	Las Vegas	Nv.	89101
Mr. X. T. Hill	5757 Pine St.	Las Vegas	Nv.	89101
Mr. Y. U. Hill	5858 Maple Dr.	Las Vegas	Nv.	89101
Mr. Z. V. Hill	5959 Birch St.	Las Vegas	Nv.	89101
Mr. A. W. Hill	6060 Walnut Dr.	Las Vegas	Nv.	89101
Mr. B. X. Hill	6161 Spruce St.	Las Vegas	Nv.	89101
Mr. C. Y. Hill	6262 Ash Ave.	Las Vegas	Nv.	89101
Mr. D. Z. Hill	6363 Hickory St.	Las Vegas	Nv.	89101
Mr. E. A. Hill	6464 Willow Dr.	Las Vegas	Nv.	89101
Mr. F. B. Hill	6565 Cherry St.	Las Vegas	Nv.	89101
Mr. G. C. Hill	6666 Elm St.	Las Vegas	Nv.	89101
Mr. H. D. Hill	6767 Oak Ave.	Las Vegas	Nv.	

- [illegible]

[illegible][illegible][illegible]

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Arg Leu Ile Asn Lys Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys
      180      185      190
Ile Ala Ala Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn
      195      200      205
Ala Gln Asp Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly
      210      215      220
Leu Asn Ser Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu
      225      230      235      240
Gly Ala Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu
      245      250      255
Gly Gly Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro
      260      265      270
Leu Thr Ala Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg
      275      280      285
His Phe Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln
      290      295      300
Val Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val
      305      310      315      320
Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala
      325      330      335
Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln
      340      345      350
Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp
      355      360      365
Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg
      370      375      380
Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp
      385      390      395      400
Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln
      405      410      415
Ala Glu Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp
      420      425      430
Glu Gly Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys
      435      440      445
Glu Leu Arg
      450

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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
  1          5          10          15
Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
      20          25          30
Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
      35          40          45
Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
      50          55          60

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Phe	Thr	Leu	Val	Ala	Ile	Leu	Leu	His	Gly	Met	Lys	Thr	Ser	Asp	Thr
65					70					75					80
Ile	Ile	Arg	Glu	Gly	Thr	Leu	Met	Gly	Thr	Ala	Ile	Gly	Thr	Cys	Phe
			85						90					95	
Gly	Tyr	Trp	Leu	Gly	Val	Ser	Ser	Phe	Ile	Tyr	Phe	Leu	Ala	Tyr	Leu
			100					105					110		
Cys	Asn	Ala	Gln	Ile	Thr	Met	Leu	Gln	Met	Leu	Ala	Leu	Leu	Gly	Tyr
		115					120					125			
Gly	Leu	Phe	Gly	His	Cys	Ile	Val	Leu	Phe	Ile	Thr	Tyr	Asn	Ile	His
	130					135					140				
Leu	His	Ala	Leu	Phe	Tyr	Leu	Phe	Trp	Leu	Leu	Val	Gly	Gly	Leu	Ser
145					150				155						160
Thr	Leu	Arg	Met	Val	Ala	Val	Leu	Val	Ser	Arg	Thr	Val	Gly	Pro	Thr
			165						170					175	
Gln	Arg	Leu	Leu	Leu	Cys	Gly	Thr	Leu	Ala	Ala	Leu	His	Met	Leu	Phe
		180						185					190		
Leu	Leu	Tyr	Leu	His	Phe	Ala	Tyr	His	Lys	Val	Val	Glu	Gly	Ile	Leu
	195						200					205			
Asp	Thr	Leu	Glu	Gly	Pro	Asn	Ile	Pro	Pro	Ile	Gln	Arg	Val	Pro	Arg
	210					215					220				
Asp	Ile	Pro	Ala	Met	Leu	Pro	Ala	Ala	Arg	Leu	Pro	Thr	Thr	Val	Leu
225					230				235						240
Asn	Ala	Thr	Ala	Lys	Ala	Val	Ala	Val	Thr	Leu	Gln	Ser	His		
				245					250						

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Gly	Ser	Glu	Asn	Glu	Ala	Leu	Asp	Leu	Ser	Met	Lys	Ser	Val	Pro
1				5				10						15	
Trp	Leu	Lys	Ala	Gly	Glu	Val	Ser	Pro	Pro	Ile	Phe	Gln	Glu	Asp	Ala
			20					25					30		
Ala	Leu	Asp	Leu	Ser	Val	Ala	Ala	His	Arg	Lys	Ser	Glu	Pro	Pro	Pro
		35				40						45			
Glu	Thr	Leu	Tyr	Asp	Ser	Gly	Ala	Ser	Val	Asp	Ser	Ser	Gly	His	Thr
	50					55				60					
Val	Met	Glu	Lys	Leu	Pro	Ser	Gly	Met	Glu	Ile	Ser	Phe	Ala	Pro	Ala
65					70				75					80	
Thr	Ser	His	Glu	Ala	Pro	Ala	Met	Met	Asp	Ser	His	Ile	Ser	Ser	Ser
			85						90					95	
Asp	Ala	Ala	Thr	Glu	Met	Leu	Ser	Gln	Pro	Asn	His	Pro	Ser	Gly	Glu
			100					105					110		
Val	Lys	Ala	Glu	Asn	Asn	Ile	Glu	Met	Val	Gly	Glu	Ser	Gln	Ala	Ala
		115					120					125			
Lys	Val	Ile	Val	Ser	Val	Glu	Asp	Ala	Val	Pro	Thr	Ile	Phe	Cys	Gly
	130					135					140				
Lys	Ile	Lys	Gly	Leu	Ser	Gly	Val	Ser	Thr	Lys	Asn	Phe	Ser	Phe	Lys
145					150				155						160

Arg	Glu	Asp	Ser	Val	Leu	Gln	Gly	Tyr	Asp	Ile	Asn	Ser	Gln	Gly	Glu
				165					170					175	
Glu	Ser	Met	Gly	Asn	Ala	Glu	Pro	Leu	Arg	Lys	Pro	Ile	Lys	Asn	Arg
			180					185					190		
Ser	Ile	Lys	Leu	Lys	Lys	Val	Asn	Ser	Gln	Glu	Val	His	Met	Leu	Pro
		195					200					205			
Ile	Lys	Lys	Gln	Arg	Leu	Ala	Thr	Phe	Phe	Pro	Arg	Lys			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys
1				5					10					15	
Lys	Asp	Glu	Pro	Lys	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
			20					25					30		
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
		35					40					45			
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
	50					55					60				
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
65					70				75					80	
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
			85						90				95		
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
		100						105					110		
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Glu	Val	Glu
	115						120					125			
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
	130					135					140				
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
145					150					155				160	
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
			165					170					175		
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr
		180						185					190		
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
	195						200					205			
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
	210					215					220				
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
225					230					235				240	
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
			245						250					255	
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
		260						265							

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Pro	Thr	Gly	Asp	Phe	Asp	Ser	Lys	Pro	Ser	Trp	Ala	Asp	Gln	Val
1				5					10					15	
Glu	Glu	Glu	Gly	Glu	Asp	Asp	Lys	Cys	Val	Thr	Ser	Glu	Leu	Leu	Lys
			20					25					30		
Gly	Ile	Pro	Leu	Ala	Thr	Gly	Asp	Thr	Ser	Pro	Glu	Pro	Glu	Leu	Leu
		35					40					45			
Pro	Gly	Ala	Pro	Leu	Pro	Pro	Pro	Lys	Glu	Val	Ile	Asn	Gly	Asn	Ile
	50					55					60				
Lys	Thr	Val	Thr	Glu	Tyr	Lys	Ile	Asp	Glu	Asp	Gly	Lys	Lys	Phe	Lys
65					70					75					80
Ile	Val	Arg	Thr	Phe	Arg	Ile	Glu	Thr	Arg	Lys	Ala	Ser	Lys	Ala	Val
				85					90					95	
Ala	Arg	Arg	Lys	Asn	Trp	Lys	Lys	Phe	Gly	Asn	Ser	Glu	Phe	Asp	Pro
			100					105					110		
Pro	Gly	Pro	Asn	Val	Ala	Thr	Thr	Thr	Val	Ser	Asp	Asp	Val	Ser	Met
		115					120					125			
Thr	Phe	Ile	Thr	Ser	Lys	Glu	Asp	Leu	Asn	Cys	Gln	Glu	Glu	Glu	Asp
	130					135					140				
Pro	Met	Asn	Lys	Phe	Lys	Gly	Gln	Lys	Ile	Val	Ser	Cys	Arg	Ile	Cys
145					150					155					160
Lys	Gly	Asp	His	Trp	Thr	Thr	Arg	Cys	Pro	Tyr	Lys	Asp	Thr	Leu	Gly
			165						170					175	
Pro	Met	Gln	Lys	Glu	Leu	Ala	Glu	Gln	Leu	Gly	Leu	Ser	Thr	Gly	Glu
			180					185					190		
Lys	Glu	Lys	Leu	Pro	Gly	Glu	Leu	Glu	Pro	Val	Gln	Ala	Thr	Gln	Asn
		195					200					205			
Lys	Thr	Gly	Lys	Tyr	Val	Pro	Pro	Ser	Leu	Arg	Asp	Gly	Ala	Ser	Arg
	210					215					220				
Arg	Gly	Glu	Ser	Met	Gln	Pro	Asn	Arg	Arg	Ala	Asp	Asp	Asn	Ala	Thr
225					230					235					240
Ile	Arg	Val	Thr	Asn	Leu	Arg	Arg	Gly	His	Ala					
				245					250						

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu

1	5	10	15
Asp	Ala	Phe	Pro
20	Lys	Val	Pro
Gly	Gly	Thr	Val
35	Ser	Leu	Ile
40	Ala	Phe	Thr
45	Thr	Thr	Met
50	Ala	Leu	Leu
55	Thr	Thr	Met
60	Ala	Leu	Leu
65	Thr	Thr	Met
70	Ala	Leu	Leu
75	Thr	Thr	Met
80	Ala	Leu	Leu
85	Thr	Thr	Met
90	Ala	Leu	Leu
95	Thr	Thr	Met
100	Ala	Leu	Leu
105	Thr	Thr	Met
110	Ala	Leu	Leu
115	Thr	Thr	Met
120	Ala	Leu	Leu
125	Thr	Thr	Met
130	Ala	Leu	Leu
135	Thr	Thr	Met
140	Ala	Leu	Leu
145	Thr	Thr	Met
150	Ala	Leu	Leu
155	Thr	Thr	Met
160	Ala	Leu	Leu
165	Thr	Thr	Met
170	Ala	Leu	Leu
175	Thr	Thr	Met
180	Ala	Leu	Leu
185	Thr	Thr	Met
190	Ala	Leu	Leu
195	Thr	Thr	Met
200	Ala	Leu	Leu
205	Thr	Thr	Met
210	Ala	Leu	Leu
215	Thr	Thr	Met
220	Ala	Leu	Leu
225	Thr	Thr	Met
230	Ala	Leu	Leu
235	Thr	Thr	Met
240	Ala	Leu	Leu
245	Thr	Thr	Met
250	Ala	Leu	Leu
255	Thr	Thr	Met
260	Ala	Leu	Leu
265	Thr	Thr	Met
270	Ala	Leu	Leu
275	Thr	Thr	Met
280	Ala	Leu	Leu
285	Thr	Thr	Met
290	Ala	Leu	Leu
295	Thr	Thr	Met
300	Ala	Leu	Leu
305	Thr	Thr	Met
310	Ala	Leu	Leu
315	Thr	Thr	Met
320	Ala	Leu	Leu
325	Thr	Thr	Met
330	Ala	Leu	Leu
335	Thr	Thr	Met
340	Ala	Leu	Leu
345	Thr	Thr	Met
350	Ala	Leu	Leu
355	Thr	Thr	Met
360	Ala	Leu	Leu
365	Thr	Thr	Met
370	Ala	Leu	Leu

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met 1	Gly	Ser	Gln	His 5	Ser	Ala	Ala	Ala	Arg 10	Pro	Ser	Ser	Cys	Arg 15	Arg
Lys	Gln	Glu	Asp 20	Asp	Arg	Asp	Gly	Leu	Leu	Ala	Glu	Arg	Glu	Gln	Glu
Glu	Ala	Ile 35	Ala	Gln	Phe	Pro	Tyr 40	Val	Glu	Phe	Thr	Gly 45	Arg	Asp	Ser
Ile	Thr 50	Cys	Leu	Thr	Cys	Gln 55	Gly	Thr	Gly	Tyr	Ile 60	Pro	Thr	Glu	Gln
Val 65	Asn	Glu	Leu	Val	Ala 70	Leu	Ile	Pro	His 75	Ser	Asp	Gln	Arg	Leu	Arg 80
Pro	Gln	Arg	Thr 85	Lys	Gln	Tyr	Val	Leu	Leu 90	Ser	Ile	Leu	Leu	Cys	Leu
Leu	Ala	Ser	Gly 100	Leu	Val	Val	Phe	Phe	Leu 105	Phe	Pro	His	Ser	Val	Leu
Val	Asp 115	Asp	Asp	Gly	Ile	Lys	Val 120	Val	Lys	Val	Thr	Phe 125	Asn	Lys	Gln
Asp 130	Ser	Leu	Val	Ile	Leu	Thr 135	Ile	Met	Ala	Thr	Leu 140	Lys	Ile	Arg	Asn
Ser 145	Asn	Phe	Tyr	Thr	Val 150	Ala	Val	Thr	Ser	Leu 155	Ser	Ser	Gln	Ile	Gln 160
Tyr	Met	Asn	Thr 165	Val	Val	Ser	Thr	Tyr	Val 170	Thr	Thr	Asn	Val	Ser	Leu
Ile	Pro	Pro	Arg 180	Ser	Glu	Gln	Leu 185	Val	Asn	Phe	Thr	Gly 190	Lys	Ala	Glu
Met	Gly 195	Gly	Pro	Phe	Ser	Tyr 200	Val	Tyr	Phe	Phe	Cys 205	Thr	Val	Pro	Glu
Ile 210	Leu	Val	His	Asn	Ile	Val 215	Ile	Phe	Met	Arg	Thr 220	Ser	Val	Lys	Ile
Ser 225	Tyr	Ile	Gly	Leu 230	Met	Thr	Gln	Ser	Ser 235	Leu	Glu	Thr	His	His	Tyr 240
Val	Asp	Cys	Gly 245	Gly	Asn	Ser	Thr	Ala	Ile 250						

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Val	Thr	Cys	Phe	His	Val	Pro	Tyr	Ser	Ala	Leu	Thr	Met	Phe	Ile
1				5					10					15	
Ser	Thr	Glu	Gln	Thr	Glu	Arg	Asp	Ser	Ala	Thr	Ala	Tyr	Arg	Met	Thr
			20					25					30		
Val	Glu	Val	Leu	Gly	Thr	Val	Leu	Gly	Thr	Ala	Ile	Gln	Gly	Gln	Ile
		35					40					45			
Val	Gly	Gln	Ala	Asp	Thr	Pro	Cys	Phe	Gln	Asp	Leu	Asn	Ser	Ser	Thr
	50					55					60				
Val	Ala	Ser	Gln	Ser	Ala	Asn	His	Thr	His	Gly	Thr	Thr	Ser	His	Arg

65					70					75					80
Glu	Thr	Gln	Lys	Ala	Tyr	Leu	Leu	Ala	Ala	Gly	Val	Ile	Val	Cys	Ile
				85					90					95	
Tyr	Ile	Ile	Cys	Ala	Val	Ile	Leu	Ile	Leu	Gly	Val	Arg	Glu	Gln	Arg
			100					105					110		
Glu	Pro	Tyr	Glu	Ala	Gln	Gln	Ser	Glu	Pro	Ile	Ala	Tyr	Phe	Arg	Gly
		115					120					125			
Leu	Arg	Leu	Val	Met	Ser	His	Gly	Pro	Tyr	Ile	Lys	Leu	Ile	Thr	Gly
	130					135					140				
Phe	Leu	Phe	Thr	Ser	Leu	Ala	Phe	Met	Leu	Val	Glu	Gly	Asn	Phe	Val
145					150				155						160
Leu	Phe	Cys	Thr	Tyr	Thr	Leu	Gly	Phe	Arg	Asn	Glu	Phe	Gln	Asn	Leu
			165					170					175		
Leu	Leu	Ala	Ile	Met	Leu	Ser	Ala	Thr	Leu	Thr	Ile	Pro	Ile	Trp	Gln
			180					185					190		
Trp	Phe	Leu	Thr	Arg	Phe	Gly	Lys	Lys	Thr	Ala	Val	Tyr	Val	Gly	Ile
	195					200						205			
Ser	Ser	Ala	Val	Pro	Phe	Leu	Ile	Leu	Val	Ala	Leu	Met	Glu	Ser	Asn
	210					215					220				
Leu	Ile	Ile	Thr	Tyr	Ala	Val	Ala	Val	Ala	Ala	Gly	Ile	Ser	Val	Ala
225					230				235						240
Ala	Ala	Phe	Leu	Leu	Pro	Trp	Ser	Met	Leu	Pro	Asp	Val	Ile	Asp	Asp
			245					250						255	
Phe	His	Leu	Lys	Gln	Pro	His	Phe	His	Gly	Thr	Glu	Pro	Ile	Phe	Phe
			260				265						270		
Ser	Phe	Tyr	Val	Phe	Phe	Thr	Lys	Phe	Ala	Ser	Gly	Val	Ser	Leu	Gly
	275					280					285				
Ile	Ser	Thr	Leu	Ser	Leu	Asp	Phe	Ala	Gly	Tyr	Gln	Thr	Arg	Gly	Cys
	290				295				300						
Ser	Gln	Pro	Glu	Arg	Val	Lys	Phe	Thr	Leu	Asn	Met	Leu	Val	Thr	Met
305					310				315						320
Ala	Pro	Ile	Val	Leu	Ile	Leu	Leu	Gly	Leu	Leu	Leu	Phe	Lys	Met	Tyr
			325					330					335		
Pro	Ile	Asp	Glu	Glu	Arg	Arg	Arg	Gln	Asn	Lys	Lys	Ala	Leu	Gln	Ala
		340					345						350		
Leu	Arg	Asp	Glu	Ala	Ser	Ser	Ser	Gly	Cys	Ser	Glu	Thr	Asp	Ser	Thr
	355					360					365				
Glu	Leu	Ala	Ser	Ile	Leu										
	370														

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
1				5				10					15		
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
			20				25					30			
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu

[illegible]

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Thr	His	Pro	Gly	Thr	Gly	Asp	Ile	Ile	Ala	Val	Met	Ile	Thr	Glu
1				5					10					15	
Leu	Arg	Gly	Lys	Asp	Ile	Leu	Ser	Tyr	Leu	Glu	Lys	Asn	Ile	Ser	Val
			20					25					30		
Gln	Met	Thr	Ile	Ala	Val	Gly	Thr	Arg	Met	Pro	Pro	Lys	Asn	Phe	Ser
		35					40					45			
Arg	Gly	Ser	Leu	Val	Phe	Val	Ser	Ile	Ser	Phe	Ile	Val	Leu	Met	Ile

50		55		60
Ile Ser Ser Ala Trp	Leu Ile Phe Tyr Phe	Ile Gln Lys Ile Arg Tyr		
65	70	75	80	
Thr Asn Ala Arg Asp	Arg Asn Gln Arg Arg	Leu Gly Asp Ala Ala Lys		
	85	90	95	
Lys Ala Ile Ser Lys	Leu Thr Thr Arg Thr	Val Lys Lys Gly Asp Lys		
	100	105	110	
Glu Thr Asp Pro Asp	Phe Asp His Cys Ala	Val Cys Ile Glu Ser Tyr		
	115	120	125	
Lys Gln Asn Asp Val	Val Arg Ile Leu Pro	Cys Lys His Val Phe His		
	130	135	140	
Lys Ser Cys Val Asp	Pro Trp Leu Ser Glu	His Cys Thr Cys Pro Met		
	145	150	155	160
Cys Lys Leu Asn Ile	Leu Lys Ala Leu Gly	Ile Val Pro Asn Leu Pro		
	165	170	175	
Cys Thr Asp Asn Val	Ala Phe Asp Met Glu	Arg Leu Thr Arg Thr Gln		
	180	185	190	
Ala Val Asn Arg Arg	Ser Ala Leu Gly Asp	Leu Ala Gly Asp Asn Ser		
	195	200	205	
Leu Gly Leu Glu Pro	Leu Arg Thr Ser Gly	Ile Ser Pro Leu Pro Gln		
	210	215	220	
Asp Gly Glu Leu Thr	Pro Arg Thr Gly Glu	Ile Asn Ile Ala Val Thr		
	225	230	235	240
Lys Glu Trp Phe Ile	Ile Ala Ser Phe Gly	Leu Leu Ser Ala Leu Thr		
	245	250	255	
Leu Cys Tyr Met Ile	Ile Arg Ala Thr Ala	Ser Leu Asn Ala Asn Glu		
	260	265	270	
Val Glu Trp Phe				
	275			

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ala	Asn	Ser	Gly	Leu	Gln	Leu	Leu	Gly	Phe	Ser	Met	Ala	Leu	Leu
1				5					10					15	
Gly	Trp	Val	Gly	Leu	Val	Ala	Cys	Thr	Ala	Ile	Pro	Gln	Trp	Gln	Met
		20						25					30		
Ser	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Ile	Thr	Ala	Gln	Ala	Met	Tyr	Lys
		35				40					45				
Gly	Leu	Trp	Met	Asp	Cys	Val	Thr	Gln	Ser	Thr	Gly	Met	Met	Ser	Cys
	50					55				60					
Lys	Met	Tyr	Asp	Ser	Val	Leu	Ala	Leu	Ser	Ala	Ala	Leu	Gln	Ala	Thr
65					70				75					80	
Arg	Ala	Leu	Met	Val	Val	Ser	Leu	Val	Leu	Gly	Phe	Leu	Ala	Met	Phe
			85					90					95		
Val	Ala	Thr	Met	Gly	Met	Lys	Cys	Thr	Arg	Cys	Gly	Gly	Asp	Asp	Lys
		100						105				110			
Val	Lys	Lys	Ala	Arg	Ile	Ala	Met	Gly	Gly	Gly	Ile	Ile	Phe	Ile	Val

	115		120		125										
Ala	Gly	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ser	Trp	Tyr	Gly	His	Gln	Ile
	130					135					140				
Val	Thr	Asp	Phe	Tyr	Asn	Pro	Leu	Ile	Pro	Thr	Asn	Ile	Lys	Tyr	Glu
145					150					155					160
Phe	Gly	Pro	Ala	Ile	Phe	Ile	Gly	Trp	Ala	Gly	Ser	Ala	Leu	Val	Ile
			165					170					175		
Leu	Gly	Gly	Ala	Leu	Leu	Ser	Cys	Ser	Cys	Pro	Gly	Asn	Glu	Ser	Lys
			180					185					190		
Ala	Gly	Tyr	Arg	Ala	Pro	Arg	Ser	Tyr	Pro	Lys	Ser	Asn	Ser	Ser	Lys
	195					200						205			
Glu	Tyr														
	210														

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ile	Arg	Pro	Gln	Leu	Arg	Thr	Ala	Gly	Leu	Gly	Arg	Cys	Leu	Leu
1				5					10					15	
Pro	Gly	Leu	Leu	Leu	Leu	Leu	Val	Pro	Val	Leu	Trp	Ala	Gly	Ala	Glu
			20					25					30		
Lys	Leu	His	Thr	Gln	Pro	Ser	Cys	Pro	Ala	Val	Cys	Gln	Pro	Thr	Arg
		35					40					45			
Cys	Pro	Ala	Leu	Pro	Thr	Cys	Ala	Leu	Gly	Thr	Thr	Pro	Val	Phe	Asp
	50					55					60				
Leu	Cys	Arg	Cys	Cys	Arg	Val	Cys	Pro	Ala	Ala	Glu	Arg	Glu	Val	Cys
65					70				75					80	
Gly	Gly	Ala	Gln	Gly	Gln	Pro	Cys	Ala	Pro	Gly	Leu	Gln	Cys	Leu	Gln
			85					90					95		
Pro	Leu	Arg	Pro	Gly	Phe	Pro	Ser	Thr	Cys	Gly	Cys	Pro	Thr	Leu	Gly
			100					105					110		
Gly	Ala	Val	Cys	Gly	Ser	Asp	Arg	Arg	Thr	Tyr	Pro	Ser	Met	Cys	Ala
	115						120					125			
Leu	Arg	Ala	Glu	Asn	Arg	Ala	Ala	Arg	Arg	Leu	Gly	Lys	Val	Pro	Ala
	130					135					140				
Val	Pro	Val	Gln	Trp	Gly	Asn	Cys	Gly	Asp	Thr	Gly	Thr	Arg	Ser	Ala
145					150					155					160
Gly	Pro	Leu	Arg	Arg	Asn	Tyr	Asn	Phe	Ile	Ala	Ala	Val	Val	Glu	Lys
			165					170					175		
Val	Ala	Pro	Ser	Val	Val	His	Val	Gln	Leu	Trp	Gly	Arg	Leu	Leu	His
		180						185					190		
Gly	Ser	Arg	Leu	Val	Pro	Val	Tyr	Ser	Gly	Ser	Gly	Phe	Ile	Val	Ser
	195						200					205			
Glu	Asp	Gly	Leu	Ile	Ile	Thr	Asn	Ala	His	Val	Val	Arg	Asn	Gln	Gln
	210					215				220					
Trp	Ile	Glu	Val	Val	Leu	Gln	Asn	Gly	Ala	Arg	Tyr	Glu	Ala	Val	Val
225					230					235					240
Lys	Asp	Ile	Asp	Leu	Lys	Leu	Asp	Leu	Ala	Val	Ile	Lys	Ile	Glu	Ser

				245					250					255					
Asn	Ala	Glu	Leu	Pro	Val	Leu	Met	Leu	Gly	Arg	Ser	Ser	Asp	Leu	Arg				
				260					265					270					
Ala	Gly	Glu	Phe	Val	Val	Ala	Leu	Gly	Ser	Pro	Phe	Ser	Leu	Gln	Asn				
				275					280					285					
Thr	Ala	Thr	Ala	Gly	Ile	Val	Ser	Thr	Lys	Gln	Arg	Gly	Gly	Lys	Glu				
				290					295					300					
Leu	Gly	Met	Lys	Asp	Ser	Asp	Met	Asp	Tyr	Val	Gln	Ile	Asp	Ala	Thr				
305						310					315				320				
Ile	Asn	Tyr	Gly	Asn	Ser	Gly	Gly	Pro	Leu	Val	Asn	Leu	Asp	Gly	Asp				
				325					330					335					
Val	Ile	Gly	Val	Asn	Ser	Leu	Arg	Val	Thr	Asp	Gly	Ile	Ser	Phe	Ala				
				340					345					350					
Ile	Pro	Ser	Asp	Arg	Val	Arg	Gln	Phe	Leu	Ala	Glu	Tyr	His	Glu	His				
				355					360					365					
Gln	Met	Lys	Gly	Lys	Ala	Phe	Ser	Asn	Lys	Lys	Tyr	Leu	Gly	Leu	Gln				
				370				375					380						
Met	Leu	Ser	Leu	Thr	Val	Pro	Leu	Ser	Glu	Glu	Leu	Lys	Met	His	Tyr				
385						390					395				400				
Pro	Asp	Phe	Pro	Asp	Val	Ser	Ser	Gly	Val	Tyr	Val	Cys	Lys	Val	Val				
				405					410					415					
Glu	Gly	Thr	Ala	Ala	Gln	Ser	Ser	Gly	Leu	Arg	Asp	His	Asp	Val	Ile				
				420					425					430					
Val	Asn	Ile	Asn	Gly	Lys	Pro	Ile	Thr	Thr	Thr	Thr	Asp	Val	Val	Lys				
				435				440					445						
Ala	Leu	Asp	Ser	Asp	Ser	Leu	Ser	Met	Ala	Val	Leu	Arg	Gly	Lys	Asp				
				450			455					460							
Asn	Leu	Leu	Leu	Thr	Val	Ile	Pro	Glu	Thr	Ile	Asn								
465					470					475									

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys				
1				5					10					15					
Lys	Asp	Glu	Pro	Glu	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp				
			20						25				30						
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly				
			35				40					45							
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met				
			50			55				60									
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala				
65				70					75					80					
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp				
			85					90					95						
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr				
			100					105					110						
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Glu	Val	Glu				

	115		120		125
Phe	Ile Ser Val Pro Val	Pro Glu Phe Ala Asp	Ser Asp Pro Ala Asn		
130		135	140		
Ile Val His Asp Phe Asn	Lys Lys Leu Thr Ala Tyr	Leu Asp Leu Asn			
145		150	155		160
Leu Asp Lys Cys Tyr Val	Ile Pro Leu Asn Thr Ser	Ile Val Met Pro			
	165	170	175		
Pro Arg Asn Leu Leu Glu	Leu Leu Ile Asn Ile Lys	Ala Gly Thr Tyr			
	180	185	190		
Leu Pro Gln Ser Tyr Leu	Ile His Glu His Met Val	Ile Thr Asp Arg			
	195	200	205		
Ile Glu Asn Ile Asp His	Leu Gly Phe Phe Ile Tyr	Arg Leu Cys His			
210		215	220		
Asp Lys Glu Thr Tyr Lys	Leu Gln Arg Arg Glu Thr	Ile Lys Gly Ile			
225		230	235		240
Gln Lys Arg Glu Ala Ser	Asn Cys Phe Ala Ile Arg	His Phe Glu Asn			
	245	250	255		
Lys Phe Ala Val Glu Thr	Leu Ile Cys Ser				
	260	265			

115
 130
 145
 160
 175
 190
 205
 220
 235
 250
 265